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GenCore version 5.1.6

DM protein - protein search, using sw model

run on: January 25, 2006, 17:10:17 ; Search time 117 Seconds

(without alignments)

928.510 Million cell updates/sec

title: US-09-502-176-2

sequence: VVLSERKTKNGKNYRGTMSK... INSQVRWYCKIPSQCDSSPV 260

scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1867569 seqs, 417829326 residues

total number of hits satisfying chosen parameters: 1867569

maximum DB seq length: 0

maximum Match 0%

Minimum Match 0%

Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%

Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pipaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pipaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pipaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pipaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pipaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pipaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	score	Query Length	DB ID	Description
1	1540	100 0	260	4 US-10-131-241-61
2	1535	99.7	303	5 US-10-810-262-11
3	1535	99.7	339	3 US-09-788-142-3
4	1535	99.7	339	3 US-09-761-120-3
5	1535	99.7	339	3 US-09-335-325-3
6	1535	99.7	339	4 US-10-131-241-3
7	1535	99.7	339	4 US-10-122-066-3
8	1535	99.7	339	4 US-10-401-564-3
9	1535	99.7	339	4 US-10-401-108-3
10	1535	99.7	363	4 US-10-292-418-11
11	1535	99.7	378	3 US-09-873-676-1
12	1535	99.7	378	3 US-09-335-325-42
13	1535	99.7	378	4 US-10-131-241-42
14	1535	99.7	378	4 US-10-415-012-2
15	1535	99.7	391	4 US-10-304-287-7
16	1535	99.7	391	4 US-10-415-012-1
17	1535	99.7	391	4 US-10-735-577-7
18	1535	99.7	394	4 US-10-304-287-8
19	1535	99.7	394	4 US-10-415-012-2
20	1535	99.7	394	4 US-10-735-577-8
21	1535	99.7	484	4 US-10-135-872B-7
22	1535	99.7	567	4 US-10-741-601-413
23	1535	99.7	569	3 US-09-946-893-5
24	1535	99.7	571	3 US-09-946-893-8
25	1535	99.7	576	3 US-09-946-883-6
26	1535	99.7	579	4 US-10-749-609-7
27	1535	99.7	714	4 US-10-415-012-8

ALIGNMENTS

RESULT 1

US-10-131-241-61

; Sequence 61, Application US/10131241

; GENERAL INFORMATION:

; APPLICANT: Holiday, John W.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Regulating Angiogenesis Using Cancer Markers

; FILE REFERENCE: 05213-0344 4310-271565

; CURRENT APPLICATION NUMBER: US/10-131,241

; CURRENT FILING DATE: 2002-07-22

; PRIORITY APPLICATION NUMBER: US 09/413,049

; PRIORITY FILING DATE: 1999-10-06

; PRIORITY APPLICATION NUMBER: US 09/316,802

; PRIORITY FILING DATE: 1999-05-21

; PRIORITY APPLICATION NUMBER: US 60/086,586

; PRIORITY FILING DATE: 1998-05-22

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 61

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-131-241-61

Query Match 100.0%; Score 1540; DB 4; Length 260;

Best Local Similarity 100.0%; Prd. N. 2.1e-120;

Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 1 VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 1 DPGPCYTIDPEKRVDYCQDLCBECRMHMSGENDGKSKTMSGLEQAWDSOPHAH 120

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 1 DPGPCYTIDPEKRVDYCQDLCBECRMHMSGENDGKSKTMSGLEQAWDSOPHAH 120

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 121 GYTPSKEPNKLKONCRNPFRELPWCPTDPNPKWELCDIPRCITPPSGSGPTYQCLK 180

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 121 GYTPSKEPNKLKONCRNPFRELPWCPTDPNPKWELCDIPRCITPPSGSGPTYQCLK 180

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 181 GTGENTRGNVAVTWSCTCHWSAQPHHTERTPENFPCNLDENYCRNPDGRAPWCH 240

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 181 GTGENTRGNVAVTWSCTCHWSAQPHHTERTPENFPCNLDENYCRNPDGRAPWCH 240

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 241 TNSQVRWYCKIPSQCDSSPV 260

Qy |||||||VYLSEERKTKNGKNYRGTMSKTKNGITCQKQSSTSPPHRPRSPATPSEGLENYCNPDN 60

Db 241 TNSQVRWYCKIPSQCDSSPV 260

RESULT 2
US-10-810-262-11
; Sequence 11, Application US/10810262
; Publication No. US20040234505A1
; GENERAL INFORMATION:
; APPLICANT: NAYLOR, STUART
; APPLICANT: KINGSMAN, SUSAN MARY
; TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
; FILE REFERENCE: 674522-2029.1
; CURRENT APPLICATION NUMBER: US/10/810,262
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 09/787,562
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/GB99/03181
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/GB98/02885
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: GB 9901906.9
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: GB 9903538.8
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO: 11
; LENGTH: 303
; TYPE: PRI
; ORGANISM: Homo sapiens
; US-10-810-262-11

Query Match 99.7%; Score 1535; DB 5; Length 303;
Best Local Similarity 99.6%; Pred. No. 5 5e-120; Mismatches 0; Indels 0; Gaps 0;
Matches 259; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGKNGKNGNYRGTMSTKNGITGCKMSLGEQAWDSOPHAH 60
Db 33 VYLSECKTGKNGKNGNYRGTMSTKNGITGCKMSLGEQAWDSOPHAH 92
Qy 61 DPGQPCYTDPKRYDCLIRECBECMHSGENYDGKISKTMGSLGEQAWDSOPHAH 120
Db 93 DPGQPCYTDPKRYDCLIRECBECMHSGENYDGKISKTMGSLGEQAWDSOPHAH 152

Qy 121 GTIPSKPNKLNKKGNYCRNPDRBLRPMCFDTDPNKRWELECDIPRCITPPSSGPTQCLK 180
Db 153 GTIPSKPNKLNKKGNYCRNPDRBLRPMCFDTDPNKRWELECDIPRCITPPSSGPTQCLK 212

Qy 181 GTGENYTRGNVAVTSGHCOHSAQTHTPHTPENPKNDENTCRNPKGRAPWHT 240
Db 213 GTGENYTRGNVAVTSGHCOHSAQTHTPHTPENPKNDENYCERNPKGRAPWHT 272

Qy 241 TNSQVRMEYCKIPSCDSSPV 260
Db 273 TNSQVRMEYCKIPSCDSSPV 292

RESULT 3
US-09-788-142-3
; Sequence 3, Application US/09788142
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDER ADDRESS:
; ADDRESSE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 3033-1769

COMPUTER READABLE FORM:

RESULT 4
US-09-761-120-3
; Sequence 3, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT APPLICATION NUMBER: US/09/761,120
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309, 821
; PRIOR FILING DATE: 1999-05-11

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,735
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
FAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLogy: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiotatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
; US-09-788-142-3

Query Match 99.7%; Score 1535; DB 3; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.4e-120; Mismatches 1; Indels 0; Gaps 0;
Matches 259; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGKNGKNGNYRGTMSTKNGITGCKMSLGEQAWDSOPHAH 60
Db 61 DPGQPCYTDPKRYDCLIRECBECMHSGENYDGKISKTMGSLGEQAWDSOPHAH 120
Qy 121 GTIPSKPNKLNKKGNYCRNPDRBLRPMCFDTDPNKRWELECDIPRCITPPSSGPTQCLK 180
Db 121 GTIPSKPNKLNKKGNYCRNPDRBLRPMCFDTDPNKRWELECDIPRCITPPSSGPTQCLK 212

Qy 181 GTGENYTRGNVAVTSGHCOHSAQTHTPHTPENPKNDENTCRNPKGRAPWHT 240
Db 181 GTGENYTRGNVAVTSGHCOHSAQTHTPHTPENPKNDENYCERNPKGRAPWHT 272

Qy 241 TNSQVRMEYCKIPSCDSSPV 260
Db 241 TNSQVRMEYCKIPSCDSSPV 260

PRIOR APPLICATION NUMBER: 08/866,735
 PRIOR FILING DATE: 1997-05-30
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3
 LENGTH: 339
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-761-120-3

Query Match 99.7%; Score 1535; DB 3; Length 339;

Best Local Similarity 99.6%; Pred. No. 7.4e-120; Mismatches 0; Indels 0; Gaps 0;

Matches 259; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGKNGNYGTMSTKNGTICKQKMSSTSPPRPRSPATPSSEGLENYCRNPDN 60
 Db 1 VYLSECKTGKNGNYGTMSTKNGTICKQKMSSTSPPRPRSPATPSSEGLENYCRNPDN 60

Qy 61 DROGPWCYTTPPEKRYDCILECEBRCMHSGENYDGKISKTMSGLECQWDSDSPHAI 120
 Db 61 DROGPWCYTTPPEKRYDCILECEBRCMHSGENYDGKISKTMSGLECQWDSDSPHAI 120

Qy 121 GYIPSKPNKLNKKNYCNRNPKDRELRLPWCFTTDPNKRNELCDIPRCTTTPSSGGPTYCLK 180
 Db 121 GYIPSKPNKLNKKNYCNRNPKDRELRLPWCFTTDPNKRNELCDIPRCTTTPSSGGPTYCLK 180

Qy 181 GTGENTGRGNVAVTWSHTCOWSAQFPHTRTPENFPCKLDENYCRNPDGKRAPWCHT 240
 Db 181 GTGENTGRGNVAVTWSHTCOWSAQFPHTRTPENFPCKLDENYCRNPDGKRAPWCHT 240

Qy 241 TNSQVRWEYCKLPSCDSSPV 260
 Db 241 TNSQVRWEYCKLPSCDSSPV 260

RESULT 5
 US-09-335-325-3
 Sequence 3, Application US/09335325
 Pattern No. US20020164717A1
 GENERAL INFORMATION:

APPLICANT: Folkman, M. Juddah
 O'Reilly, Michael
 Cao, Yihai
 Sim, B. Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335,325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3799
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULAR TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: Angiostatin fragment

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-335-325-3

Query Match 99.7%; Score 1535; DB 3; Length 339;

Best Local Similarity 99.6%; Pred. No. 7.4e-120; Mismatches 0; Indels 0; Gaps 0;

Matches 259; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGKNGNYGTMSTKNGTICKQKMSSTSPPRPRSPATPSSEGLENYCRNPDN 60
 Db 1 VYLSECKTGKNGNYGTMSTKNGTICKQKMSSTSPPRPRSPATPSSEGLENYCRNPDN 60

Qy 61 DROGPWCYTTPPEKRYDCILECEBRCMHSGENYDGKISKTMSGLECQWDSDSPHAI 120
 Db 61 DROGPWCYTTPPEKRYDCILECEBRCMHSGENYDGKISKTMSGLECQWDSDSPHAI 120

Qy 121 GYIPSKPNKLNKKNYCNRNPKDRELRLPWCFTTDPNKRNELCDIPRCTTTPSSGGPTYCLK 180
 Db 121 GYIPSKPNKLNKKNYCNRNPKDRELRLPWCFTTDPNKRNELCDIPRCTTTPSSGGPTYCLK 180

Qy 181 GTGENTGRGNVAVTWSHTCOWSAQFPHTRTPENFPCKLDENYCRNPDGKRAPWCHT 240
 Db 181 GTGENTGRGNVAVTWSHTCOWSAQFPHTRTPENFPCKLDENYCRNPDGKRAPWCHT 240

Qy 241 TNSQVRWEYCKLPSCDSSPV 260
 Db 241 TNSQVRWEYCKLPSCDSSPV 260

RESULT 6
 US-10-131-241-3

Sequence 3, Application US/10131241

Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Regulating Angiogenesis Using Cancer Markers

FILE REFERENCE: 05213-0344 43170-271565

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-05-22

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-05-22

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-05-22

PRIOR APPLICATION NUMBER: US 09/413,049

RESULT 5
 US-10-131-241-3

Query Match 99.7%; Score 1535; DB 4; Length 339;

Best Local Similarity 99.6%; Pred. No. 7.4e-120; Mismatches 0; Indels 0; Gaps 0;

Matches 259; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGKNGNYGTMSTKNGTICKQKMSSTSPPRPRSPATPSSEGLENYCRNPDN 60
 Db 1 VYLSECKTGKNGNYGTMSTKNGTICKQKMSSTSPPRPRSPATPSSEGLENYCRNPDN 60

FILE REFERENCE: 05213-2151 (43170-25208)
 CURRENT APPLICATION NUMBER: US/10/402,364
 CURRENT FILING DATE: 2003-01-28
 PRIOR APPLICATION NUMBER: US/09/761,120A
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 09/309,821
 PRIOR FILING DATE: 1999-05-11
 PRIOR APPLICATION NUMBER: 08/866,735
 PRIOR FILING DATE: 1997-05-30
 NUMBER OF SEQ ID NOS: 52
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 3
 LENGTH: 339
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-402-364-3

RESULT 7
 US-10-127-066-3

; Sequence 3, Application US/10127066
; Publication No. US20030064926A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; APPLICANT: Folkman, M. Judah
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
; FILING DATE: 2002-07-23
; CURRENT APPLICATION NUMBER: US/10/127,066
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-127-066-3

Query Match 99.7%; Score 1335; DB 4; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7,4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBCKTGNGKNGRTGMSKTKNGITCOKWMSSTSPHRPRSPATHPSGLEENYCRNPDN 60
 Db 1 VYLSBCKTGNGKNGRTGMSKTKNGITCOKWMSSTSPHRPRSPATHPSGLEENYCRNPDN 60

Qy 61 DPGQWCYTDPKRYDQDLCERBCMHMSGENDGKISKTMGLECOMDSOPHAH 120
 Db 61 DPGQWCYTDPKRYDQDLCERBCMHMSGENDGKISKTMGLECOMDSOPHAH 120

Qy 121 GYIPSKFPNKLKKYCRNDRERLPWCFTDPNKRWLCDIPRCTTPPSGGTYQCLK 180
 Db 121 GYIPSKFPNKLKKYCRNDRERLPWCFTDPNKRWLCDIPRCTTPPSGGTYQCLK 180

Qy 181 GTGENRGNVAVTWSHTCOWHSACTPHTHTPENPKCNLDENYCRNPDGKAPWCHT 240
 Db 181 GTGENRGNVAVTWSHTCOWHSACTPHTHTPENPKCNLDENYCRNPDGKAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9
 US-10-401-108-3

; Sequence 3, Application US/10401108
; Publication No. US20040023877A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/401,108
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,735
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714

RESULT 8
 US-10-402-364-3
; Sequence 3, Application US/10402364
; Publication No. US20040002459A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael
; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen

REFERENCE/DOCKET NUMBER: 05940-0129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 818-3700
 FAX: (404) 818-3799
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 STRANDBEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Angiostatin fragment
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-10-401-108-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7, 4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBECTKGNGKNGYRGMSTKNGITCQKWSSTSPPHRPRSPATHSEGLEENYCRNPDN 60
 Db 2 VYLSBECTKGNGKNGYRGMSTKNGITCQKWSSTSPPHRPRSPATHSEGLEENYCRNPDN 61

Qy 61 DPGPWCYTDPERKRYDCDIECEBCMHSGENYDGKSKTMSGIECQWDSOPRAH 120
 Db 62 DPGPWCYTDPERKRYDCDIECEBCMHSGENYDGKSKTMSGIECQWDSOPRAH 121

Qy 121 GYPSKEPNKLNKRNCPDRELRLPWCFTTDPKWELCDIPRCCTTPPSGGPTQCLK 180
 Db 122 GYPSKEPNKLNKRNCPDRELRLPWCFTTDPKWELCDIPRCCTTPPSGGPTQCLK 181

Qy 181 GTGENTRGNVAVTVSGHTCQHSAQTPHTPRTTPENPKCQNDENYCRNPDKRAPWCHT 240
 Db 182 GTGENTRGNVAVTVSGHTCQHSAQTPHTPRTTPENPKCQNDENYCRNPDKRAPWCHT 241

Qy 241 TNSQVRWVEYCKIPSCDSSPV 260
 Db 242 TNSQVRWVEYCKIPSCDSSPV 261

RESULT 10
 Sequence 11, Application US/1029418
 Publication No. US20030139365A1
 GENERAL INFORMATION:
 APPLICANT: MacDonald, Nicholas J.
 ATTORNEY: Sim, Kim L.
 TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
 FILE REFERENCE: 05213-0378 (4310-259333)
 CURRENT APPLICATION NUMBER: US/09/873,676
 CURRENT FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: US 60/209, 065
 PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: US 60/289, 387
 PRIOR FILING DATE: 2001-05-08
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 1
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-873,676-1

Query Match 99.7%; Score 1535; DB 3; Length 378;
 Best Local Similarity 99.6%; Pred. No. 8, 4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBECTKGNGKNGYRGMSTKNGITCQKWSSTSPPHRPRSPATHSEGLEENYCRNPDN 60
 Db 6 VYLSBECTKGNGKNGYRGMSTKNGITCQKWSSTSPPHRPRSPATHSEGLEENYCRNPDN 65

Qy 61 DPGPWCYTDPERKRYDCDIECEBCMHSGENYDGKSKTMSGIECQWDSOPRAH 120
 Db 66 DPGPWCYTDPERKRYDCDIECEBCMHSGENYDGKSKTMSGIECQWDSOPRAH 125

Qy 121 GYPSKEPNKLNKRNCPDRELRLPWCFTTDPKWELCDIPRCCTTPPSGGPTQCLK 180
 Db 126 GYPSKEPNKLNKRNCPDRELRLPWCFTTDPKWELCDIPRCCTTPPSGGPTQCLK 185

Qy 181 GTGENTRGNVAVTVSGHTCQHSAQTPHTPRTTPENPKCQNDENYCRNPDKRAPWCHT 240
 Db 186 GTGENTRGNVAVTVSGHTCQHSAQTPHTPRTTPENPKCQNDENYCRNPDKRAPWCHT 245

Qy 241 TNSQVRWVEYCKIPSCDSSPV 260
 Db 246 TNSQVRWVEYCKIPSCDSSPV 265

RESULT 12
 Best Local Similarity 99.6%; Pred. No. 8e-120;
 US-10-292-418-11

Query Match 99.7%; Score 1535; DB 4; Length 363;
 Best Local Similarity 99.6%; Pred. No. 8e-120;
 US-09-335-325-42

Sequence 42, Application US/09335325
 Patent No. US2002016477A1
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 O'Reilly, Michael S.
 Cao, Yihai
 Sim, B. Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Akew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 09/335,325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: K1-48KLIS
 ;
 SBQUENCE DESCRIPTION: SEQ ID NO: 42:
 US-09-335-325-42

Query Match 99.7%; Score 1535; DB 3; Length 378;
 Best Local Similarity 99.6%; Pred. No. 8.4e-10; Indels 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY  1 VVLSECKTGKNGKNGTMSKTKGNGTCKQKSSTSPPHRPRSPATHPSEGLENCRNPDN 60
Db   6 VVLSECKTGKNGKNGTMSKTKGNGTCKQKSSTSPPHRPRSPATHPSEGLENCRNPDN 65
QY  61 DPGGPWCYTDPERKRYDYCOTLECEBECMCSGENYDGKISKTMGGLCQAWDSOPHAN 120
Db   66 DPQGPWCYTDPERKRYDYCILCEBECMCSGENYDGKISKTMGGLCQAWDSOPHAN 125
QY  121 GYIPSKFPNKLNKQYCNRNDPDRLLPWFCDPRTTPPSGGPTVCLK 180
Db   126 GYIPSKFPNKLNKQYCNRNDPDRLLPWFCDPRTTPPSGGPTVCLK 185
QY  181 GTGENYRGNAVTWSGTQHWAQTPHTHTPENPCTGNDLWYCRNDGKRAPWHT 240
Db   186 GTGENYRGNAVTWSGTQHWAQTPHTHTPENPCTGNDLWYCRNDGKRAPWHT 245
QY  241 TNSQVRWYCKLPSCDSSPV 260
Db   246 TNSQVRWYCKLPSCDSSPV 265

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RESULT 14
 US-10-127-066-42
 ; Sequence 42, Application US/10127066
 ; Publication No. US2003006426A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Reilly, Michael S.
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, Kim Lee
 ; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 ; FILE REFERENCE: 05213-0612 4310-22529
 ; CURRENT APPLICATION NUMBER: US10/127-066
 ; CURRENT FILING DATE: 2002-07-23
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 42
 ; LENGTH: 378
 ; TYPE: PRT

241 TNSQVRWYCKLPSCDSSPV 260

; ORGANISM: Homo sapiens
US-10-127-066-42

Query Match 99.7%; Score 1535; DB 4; Length 378;

Best Local Similarity 99.6%; Pred. No. 8.4e-120; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLSBECKTGNGKNYRGTMKTKGNTQKWAESTSPHRPRSPATHSEGLENRYCRNPDN 60

Db 6 VVLSBECKTGNGKNYRGTMKTKGNTQKWAESTSPHRPRSPATHSEGLENRYCRNPDN 65

QY 61 DPGPWCYTTPDEKRYCQDILCEBECMHSGENYKGKISKUMSGLECOAWSQPHAH 120

Db 66 DPGPWCYTTPDEKRYCQDILCEBECMHSGENYKGKISKUMSGLECOAWSQPHAH 125

QY 121 GTIPSKEPNKNUKKKTCRNPDRBLRPCFTDPNKWELCIPRCTTPSSGPTQCLK 180

Db 126 GTIPSKEPNKNUKKKTCRNPDRBLRPCFTDPNKWELCIPRCTTPSSGPTQCLK 185

QY 181 GTGENTYGRNVAVTVSQHICQWMSAQTPHTHTERTPENPCKNDENYCRNPDKRAFWCHT 240

Db 186 GTGENTYGRNVAVTVSQHICQWMSAQTPHTHTERTPENPCKNDENYCRNPDKRAFWCHT 245

QY 241 TNSQVRMEYCKIPSCDSSPV 260

Db 246 TNSQVRMEYCKIPSCDSSPV 265

RESULT 15

US-10-304-287-7
Sequence 7, Application US/10304287

PUBLICATION NO. US2003008323A1

GENERAL INFORMATION:

APPLICANT: Weisman, David M.

APPLICANT: Kwon, Mijung

TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor

FILE REFERENCE: WO02-001

CURRENT APPLICATION NUMBER: US/10/304,287

CURRENT FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: US 60/333,866

PRIOR FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Microsoft Word

SEQ ID NO: 7

TYPE: PRT

LENGTH: 391

ORGANISM: mammalian

US-10-304-287-7

Query Match 99.7%; Score 1535; DB 4; Length 391;
Best Local Similarity 99.6%; Pred. No. 8.7e-120; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLSBECKTGNGKNYRGTMKTKGNTQKWAESTSPHRPRSPATHSEGLENRYCRNPDN 60

Db 2 VVLSBECKTGNGKNYRGTMKTKGNTQKWAESTSPHRPRSPATHSEGLENRYCRNPDN 65

QY 61 DPGPWCYTTPDEKRYCQDILCEBECMHSGENYKGKISKUMSGLECOAWSQPHAH 120

Db 62 DPGPWCYTTPDEKRYCQDILCEBECMHSGENYKGKISKUMSGLECOAWSQPHAH 125

QY 121 GTIPSKEPNKNUKKKTCRNPDRBLRPCFTDPNKWELCIPRCTTPSSGPTQCLK 180

Db 122 GTIPSKEPNKNUKKKTCRNPDRBLRPCFTDPNKWELCIPRCTTPSSGPTQCLK 185

QY 181 GTGENTYGRNVAVTVSQHICQWMSAQTPHTHTERTPENPCKNDENYCRNPDKRAFWCHT 240

Db 182 GTGENTYGRNVAVTVSQHICQWMSAQTPHTHTERTPENPCKNDENYCRNPDKRAFWCHT 245

QY 241 TNSQVRMEYCKIPSCDSSPV 260

Db 242 TNSQVRMEYCKIPSCDSSPV 265

Search completed: January 25, 2006, 17:21:52
Job time : 118 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:04:06 ; Search time 45 Seconds
 Sequence: 1 VYLSECKTGNGKNYRGTMNSK.....TNSQVRWBYCKLPSQCDSSPV 260
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Title: US-09-502-176-2
 Perfect score: 1540
 Sequence: 1 VYLSECKTGNGKNYRGTMNSK.....TNSQVRWBYCKLPSQCDSSPV 260

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/prodata/1/aa/5_COMB_pep:
 2: /cgn2_6/prodata/1/aa/H_COMB_pep:
 3: /cgn2_6/prodata/1/aa/Ctctus_COMB_pep:
 4: /cgn2_6/prodata/1/aa/RE_COMB_pep:
 5: /cgn2_6/prodata/1/aa/backfiles1_pep:
 6: /cgn2_6/prodata/1/aa/backfiles1_pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1540	100.0	260	2 US-09-982-516-1	Sequence 1, Appli
2	1535	99.7	339	1 US-08-248-629A-3	Sequence 3, Appli
3	1535	99.7	339	1 US-08-451-932-3	Sequence 3, Appli
4	1535	99.7	339	1 US-08-452-200-3	Sequence 3, Appli
5	1535	99.7	339	1 US-08-326-785-3	Sequence 3, Appli
6	1535	99.7	339	1 US-08-612-788-3	Sequence 3, Appli
7	1535	99.7	339	1 US-08-605-988B-3	Sequence 3, Appli
8	1535	99.7	339	1 US-08-429-743-3	Sequence 3, Appli
9	1535	99.7	339	1 US-08-866-735-3	Sequence 3, Appli
10	1535	99.7	339	2 US-09-066-038-3	Sequence 3, Appli
11	1535	99.7	339	2 US-09-335-225-3	Sequence 3, Appli
12	1535	99.7	339	2 US-09-335-614-3	Sequence 3, Appli
13	1535	99.7	339	4 PCT-US95-0507-3	Sequence 3, Appli
14	1535	99.7	374	2 US-09-377-250-3	Sequence 3, Appli
15	1535	99.7	375	2 US-09-377-250-2	Sequence 3, Appli
16	1535	99.7	378	1 US-08-612-788-42	Sequence 4, Appli
17	1535	99.7	378	2 US-09-066-028-42	Sequence 42, Appli
18	1535	99.7	378	2 US-09-206-559-1	Sequence 1, Appli
19	1535	99.7	378	2 US-09-335-325-42	Sequence 3, Appli
20	1535	99.7	378	2 US-09-335-614-42	Sequence 42, Appli
21	1535	99.7	451	2 US-09-377-250-1	Sequence 1, Appli
22	1535	99.7	452	2 US-09-377-250-4	Sequence 4, Appli
23	1535	99.7	452	2 US-08-469-866-54	Sequence 54, Appli
24	1535	99.7	790	1 US-08-469-588-54	Sequence 54, Appli
25	1535	99.7	791	1 US-08-643-219-1	Sequence 1, Appli
26	1535	99.7	791	1 US-09-131-995-1	Sequence 1, Appli
27	99.7	791	1 US-08-832-087B-1	Db	

ALIGNMENTS

Query Match	Score	Length
Best Local Similarity	100.0%	Score 1540, DB 2, Length 260;
Matches	0	Pred. No. 3.3e-139; Mismatches 0; Indels 0; Gaps 0;
Qry	1 VYLSECKTGNGKNYRGTMNSKTKNGTCKQWSSTSPPRPRSPATPSSEGLENYCRNPDN 60	Db 1 VYLSECKTGNGKNYRGTMNSKTKNGTCKQWSSTSPPRPRSPATPSSEGLENYCRNPDN 60
Qry	61 DPOGWCYTDPERKYDQILRCBECMIGSGENYDGKISKTMGLBCQAWDSQPHN 120	Db 61 DPOGWCYTDPERKYDQILRCBECMIGSGENYDGKISKTMGLBCQAWDSQPHN 120
Qry	121 GYPSKPKNPKNYCRMPDRPCLPCKTPDKRWEQDIPCTTPRSSGTYQCK 180	Db 121 GYPSKPKNPKNYCRMPDRPCLPCKTPDKRWEQDIPCTTPRSSGTYQCK 180
Qry	121 GYPSKPKNPKNYCRMPDRPCLPCKTPDKRWEQDIPCTTPRSSGTYQCK 180	Db 121 GYPSKPKNPKNYCRMPDRPCLPCKTPDKRWEQDIPCTTPRSSGTYQCK 180
Qry	181 GTGENYGRNVAVTSGHTCQHMSAQTPHTHERTENPCKNLDENYCRPDKGAPWCH 240	Db 181 GTGENYGRNVAVTSGHTCQHMSAQTPHTHERTENPCKNLDENYCRPDKGAPWCH 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 2
US-08-248-629A-3
; Sequence 3, Application US/08248629A
; Patent No. 5639725
; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; TITLE OF INVENTION: Angiostatin and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,629A
FILING DATE: 04/26/94
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 05213-0120

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,932
FILING DATE: 05/26/95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0123

TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
TOPOLOGY: linear

US-08-248-629A-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGTGTGMSKTKNGTQKGTSKQKNSSTSPHRPRSPATHPSEGLENYCNPDN 60
Db 1 VYLSECKTGNGKNGTGTGMSKTKNGTQKGTSKQKNSSTSPHRPRSPATHPSEGLENYCNPDN 60

Qy 61 DPOGPWCYTDPERKRYCDILCEBECMHSGENGDGKTSKTMGLECQWDSDOSPNAH 120
Db 61 DPOGPWCYTDPERKRYCDILCEBECMHSGENGDGKTSKTMGLECQWDSDOSPNAH 120

Qy 121 GYIPSKEPKNKLKKNYCNPDRSLPCKFTTDENPKRBLCDIPRCTTPPSGGPTYQCLK 180
Db 121 GYIPSKEPKNKLKKNYCNPDRSLPCKFTTDENPKRBLCDIPRCTTPPSGGPTYQCLK 180

Qy 121 GYIPSKEPKNKLKKNYCNPDRSLPCKFTTDENPKRBLCDIPRCTTPPSGGPTYQCLK 180
Db 121 GYIPSKEPKNKLKKNYCNPDRSLPCKFTTDENPKRBLCDIPRCTTPPSGGPTYQCLK 180

Qy 181 GTGENGYRNVAVTSGHTQHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240
Db 181 GTGENGYRNVAVTSGHTQHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 3
US-08-451-932-3
; Sequence 3, Application US/08451932
; Patent No. 5733876
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Method of Treating an Angiogenic Disease
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,932
FILING DATE: 05/26/95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0123

TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
TOPOLOGY: linear

US-08-451-932-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGTGTGMSKTKNGTQKGTSKQKNSSTSPHRPRSPATHPSEGLENYCNPDN 60
Db 1 VYLSECKTGNGKNGTGTGMSKTKNGTQKGTSKQKNSSTSPHRPRSPATHPSEGLENYCNPDN 60

Qy 61 DPOGPWCYTDPERKRYCDILCEBECMHSGENGDGKTSKTMGLECQWDSDOSPNAH 120
Db 61 DPOGPWCYTDPERKRYCDILCEBECMHSGENGDGKTSKTMGLECQWDSDOSPNAH 120

Qy 121 GYIPSKEPKNKLKKNYCNPDRSLPCKFTTDENPKRBLCDIPRCTTPPSGGPTYQCLK 180
Db 121 GYIPSKEPKNKLKKNYCNPDRSLPCKFTTDENPKRBLCDIPRCTTPPSGGPTYQCLK 180

Qy 181 GTGENGYRNVAVTSGHTQHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240
Db 181 GTGENGYRNVAVTSGHTQHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 4
US-08-452-260-3
; Sequence 3, Application US/08452260
; Patent No. 5776704
; GENERAL INFORMATION:

APPLICANT: Folkman, Judah
 APPLICANT: O'Reilly, Michael
 TITLE OF INVENTION: Method of Diagnosing an Angiogenic Disease
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA

ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7.0
 SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/452,260
 FILING DATE: 05/26/95
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/248,629
 FILING DATE: 04/26/94

ATTORNEY/AGENT INFORMATION:
 NAME: Harry W. Stults, Ph.D.
 REGISTRATION NUMBER: 34,025
 REFERENCE/DOCKET NUMBER: 0213-0124

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEX/FAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339

TYPE: amino acid
 TOPOLOGY: linear

US-08-452-260-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGKNGYRGTMISKKGITCQKMSSTSPPHRPRFSPATHSEGLENYCRPNP
 Db 1 VYLSECKTGNGKNGYRGTMISKKGITCQKMSSTSPPHRPRFSPATHSEGLENYCRPNP
 QY 61 DPOGPWCYTDPBKRYDCLIECEBECMHSGENYDGKISKTMSGLECOAWDSOPHAA
 Db 61 DPOGPWCYTDPBKRYDCLIECEBECMHSGENYDGKISKTMSGLECOAWDSOPHAA 60
 QY 121 GYIPSKEPNPKLKKYCRNPRLRWCFTDPNPKWELCIPRCCTTPSSGPTVQCLK 180
 Db 121 GYIPSKEPNPKLKKYCRNPRLRWCFTDPNPKWELCDIPRCCTTPSSGPTVQCLK 180
 QY 181 GTGENYTRGNVAVTVSGHTCQWSAQTPHTHTPENFPCKOLDENYCRNPDKRAPWCHT 240
 Db 181 GTGENYTRGNVAVTVSGHTCQWSAQTPHTHTPENFPCKOLDENYCRNPDKRAPWCHT 240
 QY 241 TNSQVREYCKIPSCDSPPV 260
 Db 241 TNSQVREYCKIPSCDSPPV 260

RESULT 6

US-08-612-788-3

; Sequence 3, Application US/08612788
 ; Patent No. 5837682

GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael

APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
 ADDRESSE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia

ADDRESSE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA

ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7.0
 SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/326,785
 FILING DATE:
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/248,629
 FILING DATE: 04/26/94

ATTORNEY/AGENT INFORMATION:
 NAME: Harry W. Stults, Ph.D.
 REGISTRATION NUMBER: 34,025
 REFERENCE/DOCKET NUMBER: 0213-0121

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEX/FAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339

TYPE: amino acid
 TOPOLOGY: linear

US-08-326-785-3

Query Match 99.7%; Score 1535; DB 1; Length 339;

Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMISKKGITCQKMSSTSPPHRPRFSPATHSEGLENYCRPNP
 Db 1 VYLSECKTGNGKNGYRGTMISKKGITCQKMSSTSPPHRPRFSPATHSEGLENYCRPNP 60

QY 61 DPOGPWCYTDPBKRYDCLIECEBECMHSGENYDGKISKTMSGLECOAWDSOPHAA 120

Db 61 DPOGPWCYTDPBKRYDCLIECEBECMHSGENYDGKISKTMSGLECOAWDSOPHAA 120

QY 121 GYIPSKEPNPKLKKYCRNPRLRWCFTDPNPKWELCIPRCCTTPSSGPTVQCLK 180

Db 121 GYIPSKEPNPKLKKYCRNPRLRWCFTDPNPKWELCDIPRCCTTPSSGPTVQCLK 180

QY 181 GTGENYTRGNVAVTVSGHTCQWSAQTPHTHTPENFPCKOLDENYCRNPDKRAPWCHT 240

Db 181 GTGENYTRGNVAVTVSGHTCQWSAQTPHTHTPENFPCKOLDENYCRNPDKRAPWCHT 240

QY 241 TNSQVREYCKIPSCDSPPV 260

Db 241 TNSQVREYCKIPSCDSPPV 260

RESULT 5

US-08-785-3

; Sequence 3, Application US/08612788
 ; Patent No. 5837682

GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael

APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
 ADDRESSE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia

RESULT 5

US-08-326-785-3

; Sequence 3, Application US/08612788
 ; Patent No. 5837682

GENERAL INFORMATION:
 APPLICANT: Folkman, Judah

APPLICANT: O'Reilly, Michael

TITLE OF INVENTION: Angiostatin and Method of Use
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: 22-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-08-612-788-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBCKTGNGKNGYRGTMSTKNGITCOKWSSSTSPHRPRSPATHPSEGLENYCNPDN 60
Db 1 VYLSBCKTGNGKNGYRGTMSTKNGITCOKWSSSTSPHRPRSPATHPSEGLENYCNPDN 60
Qy 61 DPGGPWCYTTPDKRVDYLRCERCMHCSGENYDCKSKTMGLCQAWDSQPHAH 120
Db 61 DPGGPWCYTTPDKRVDYLRCERCMHCSGENYDCKSKTMGLCQAWDSQPHAH 120
Qy 121 GTYSKPSKPKNKLKKGNCYCRNPDRLPWCFTDPNKKWELCDIPRCTTPSSGPTYCLK 180
Db 121 GTYSKPSKPKNKLKKGNCYCRNPDRLPWCFTDPNKKWELCDIPRCTTPSSGPTYCLK 180
Qy 181 GTGENTGRVAVTVSHTCOHWSAQTPRHERTPENFFCKNDENYCRNPDGKRAPWHT 240
Db 181 GTGENTGRVAVTVSHTCOHWSAQTPRHERTPENFFCKNDENYCRNPDGKRAPWHT 240
Qy 241 TNSQVRWEYCKIPSCDSPV 260
Db 241 TNSQVRWEYCKIPSCDSPV 260

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBCKTGNGKNGYRGTMSTKNGITCOKWSSSTSPHRPRSPATHPSEGLENYCNPDN 60

Db 1 VYLSBCKTGNGKNGYRGTMSTKNGITCOKWSSSTSPHRPRSPATHPSEGLENYCNPDN 60

Qy 61 DPGGPWCYTTPDKRVDYLRCERCMHCSGENYDCKSKTMGLCQAWDSQPHAH 120

Db 61 DPGGPWCYTTPDKRVDYLRCERCMHCSGENYDCKSKTMGLCQAWDSQPHAH 120

Qy 121 GTYSKPSKPKNKLKKGNCYCRNPDRLPWCFTDPNKKWELCDIPRCTTPSSGPTYCLK 180

Db 121 GTYSKPSKPKNKLKKGNCYCRNPDRLPWCFTDPNKKWELCDIPRCTTPSSGPTYCLK 180

Qy 181 GTGENTGRVAVTVSHTCOHWSAQTPRHERTPENFFCKNDENYCRNPDGKRAPWHT 240

Db 181 GTGENTGRVAVTVSHTCOHWSAQTPRHERTPENFFCKNDENYCRNPDGKRAPWHT 240

Qy 241 TNSQVRWEYCKIPSCDSPV 260

Db 241 TNSQVRWEYCKIPSCDSPV 260

RESULT 7
US-08-605-598B-3
Sequence 3 Application US/08605598B
Patent No. 5861372
GENERAL INFORMATION:
APPLICANT: Folkmann, M. Judah
APPLICANT: Lin, Jie
APPLICANT: O'Reilly, Michael S.
TITLE OF INVENTION: Aggregate Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: United States
ZIP: 30303-1769

RESULT 8
US-08-429-743-3
; Sequence 3, Application US/08429743
; Patent No. 5885795
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; APPLICANT: Folkmann, M. Judah
; APPLICANT: Sim, Kim Lee
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Angiostatin and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: United States
; ZIP: 30303-1769

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,743
 FILING DATE: 26-APR-1994
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,629
 FILING DATE: 26-APR-1994
 REFERENCE/DOCKET NUMBER: 05213-0122
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US 08/326,785
 ATTORNEY/AGENT INFORMATION:
 NAME: Johnson, James D.
 REGISTRATION NUMBER: 31,771
 TELEPHONE: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 ;
 US-08-429-743-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSCKERGNGKNYRGTMKTINGITCKQKVSSTSPHRPRSPATHSSEGLENVCRNPDN 60
 Db 1 VYLSCKERGNGKNYRGTMKTINGITCKQKVSSTSPHRPRSPATHSSEGLENVCRNPDN 60
 Qy 61 DPQGPWCYTDPBKRYCDILCECERCMHCSGENYDGKSKTMSGLEQAWDSOPHAK 120
 Db 61 DPQGPWCYTDPBKRYCDILCECERCMHCSGENYDGKSKTMSGLEQAWDSOPHAK 120
 Qy 121 GYIPSKEPNPKLNKRNKRNPKDRELRLPWCFTTDPNKRNWLCDIPRCTTPPSGGPTYCLK 180
 Db 121 GYIPSKEPNPKLNKRNKRNPKDRELRLPWCFTTDPNKRNWLCDIPRCTTPPSGGPTYCLK 180
 Qy 181 GTGENTRGNVAVTVSGHTCOWSAQTPTHTPRTPEPCKQDNLDENYCRNPDKGRAFWHT 240
 Db 181 GTGENTRGNVAVTVSGHTCOWSAQTPTHTPRTPEPCKQDNLDENYCRNPDKGRAFWHT 240
 Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 241 TNSQVRWEYCKIPSCDSSPV 260

COUNTRY: USA
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/866,735
 FILING DATE: 30-MAY-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05940-0129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 818-3700
 TELEFAX: (404) 818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Angiotatin fragment
 ;
 US-08-866-735-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSCKERGNGKNYRGTMKTINGITCKQKVSSTSPHRPRSPATHSSEGLENVCRNPDN 60
 Db 1 VYLSCKERGNGKNYRGTMKTINGITCKQKVSSTSPHRPRSPATHSSEGLENVCRNPDN 60
 Qy 61 DPQGPWCYTDPBKRYCDILCECERCMHCSGENYDGKSKTMSGLEQAWDSOPHAK 120
 Db 61 DPQGPWCYTDPBKRYCDILCECERCMHCSGENYDGKSKTMSGLEQAWDSOPHAK 120
 Qy 121 GYIPSKEPNPKLNKRNKRNPKDRELRLPWCFTTDPNKRNWLCDIPRCTTPPSGGPTYCLK 180
 Db 121 GYIPSKEPNPKLNKRNKRNPKDRELRLPWCFTTDPNKRNWLCDIPRCTTPPSGGPTYCLK 180
 Qy 181 GTGENTRGNVAVTVSGHTCOWSAQTPTHTPRTPEPCKQDNLDENYCRNPDKGRAFWHT 240
 Db 181 GTGENTRGNVAVTVSGHTCOWSAQTPTHTPRTPEPCKQDNLDENYCRNPDKGRAFWHT 240
 Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9
 US-08-866-735-3
 ; Sequence 3, Application US/08866735
 ; Patent No. 5545403
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; TITLE OF INVENTION: Anglostatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew, LLP
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia

RESULT 10
 US-09-066-028-3
 ; Sequence 3, Application US/09066028
 ; Patent No. 6024688
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/066,028

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/612,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05213-0126

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/066,028

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/612,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05213-0126

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TOPOLOGY: linear

MOLECULE TYPE: protein

Patent No. 6949511
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 O'Reilly, Michael
 Cao, Yihai
 Sim, B. Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC/DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335, 614
 FILING DATE: 18-Jun-1999
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/612, 788
 FILING DATE: 08-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Angiostatin fragment
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-09-335-614-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKNGRTGTMKNGTICQKWSSTSPPHRPRSPATHPSGLEBNYCRNPDN 60
 Db 1 VYLSECKTGKNGKNGRTGTMKNGTICQKWSSTSPPHRPRSPATHPSGLEBNYCRNPDN 60

QY 61 DPOQFWCYTIDPEKRYDYCILEBECHECMHSGENYDGKISKTMGLCQAWQSOPHAB 120
 61 DPOQFWCYTIDPEKRYDYCILEBECHECMHSGENYDGKISKTMGLCQAWQSOPHAB 120

QY 121 GYISSKPKPNLKGKNCRDPRELPWCFTDPNKGWLCDIPCTTPSSGTYQCIK 180
 121 GYISSKPKPNLKGKNCRDPRELPWCFTDPNKGWLCDIPCTTPSSGTYQCIK 180

QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTERTPENPKCKNLDENYCRNDGKAPWCHT 240
 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTERTPENPKCKNLDENYCRNDGKAPWCHT 240

Db 241 TNSQVRWEYCKIPSCDSPV 260
 ;|||||||||||||||||||

Db 241 TNSQVRWEYCKIPSCDSPV 260
 RESULT 13
 PCT-US95-05107-3
 ; Sequence 3 Application PC/TUS9505107
 GENERAL INFORMATION:
 APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION
 TITLE OF INVENTION: Angiostatin and Method of Use
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC/DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05107
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/248, 629
 FILING DATE: 26-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Johnson, James D.
 REGISTRATION NUMBER: 31,771
 REFERENCE/DOCKET NUMBER: 05213-0122
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 PCT-US95-05107-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKNGRTGTMKNGTICQKWSSTSPPHRPRSPATHPSGLEBNYCRNPDN 60
 Db 1 VYLSECKTGKNGKNGRTGTMKNGTICQKWSSTSPPHRPRSPATHPSGLEBNYCRNPDN 60

QY 61 DPOQFWCYTIDPEKRYDYCILEBECHECMHSGENYDGKISKTMGLCQAWQSOPHAB 120
 61 DPOQFWCYTIDPEKRYDYCILEBECHECMHSGENYDGKISKTMGLCQAWQSOPHAB 120

QY 121 GYISSKPKPNLKGKNCRDPRELPWCFTDPNKGWLCDIPCTTPSSGTYQCIK 180
 121 GYISSKPKPNLKGKNCRDPRELPWCFTDPNKGWLCDIPCTTPSSGTYQCIK 180

Db 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTERTPENPKCKNLDENYCRNDGKAPWCHT 240
 181 GTGENYRGNAVAVTSGHTCOHWSAQTPHTERTPENPKCKNLDENYCRNDGKAPWCHT 240

Db 241 TNSQVRWEYCKIPSCDSPV 260
 ;|||||||||||||||

Db 241 TNSQVRWEYCKIPSCDSSPV 260
 RESULT 14
 US-09-377-250-3
 ; Sequence 3, Application US/09377250
 ; Patent No. 6365364
 ; GENERAL INFORMATION:
 ; APPLICANT: MANN, KENNETH G.
 ; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
 ; FILE REFERENCE: 48409360
 ; CURRENT APPLICATION NUMBER: US/09/377, 250
 ; CURRENT FILING DATE: 1999-08-19
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: angiogenesis inhibitor
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (264)
 ; OTHER INFORMATION: Xaa = Gln or Glu
 ; US-09-377-250-3

; NAME/KEY: MOD RES
 ; LOCATION: (265)
 ; OTHER INFORMATION: Xaa = Gln or Glu
 ; US-09-377-250-2

Query Match 99.7%; Score 1535; DB 2; Length 375;
 Best Local Similarity 99.6%; Pred. No. 1.6e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGKNGNYRGTMSKTRGKTCOKWSSTSPPHRFRSPATHPSGLBENYCRNDN 60
 Db 2 VYLSECKTGKNGNYRGTMSKTRGKTCOKWSSTSPPHRFRSPATHPSGLBENYCRNDN 61

Qy 61 DPOGPWCYTDPERKYDIDICRCRCHCSENYDGKISKMSGLECQAMDSOPRAH 120
 Db 62 DPOGPWCYTDPERKYDIDICRCRCHCSENYDGKISKMSGLECQAMDSOPRAH 121

Qy 121 GYIPLSKFPNKLKNYCNPDRERLPWFTTDPKRMWLDIDPRCTTTPPSGGPYQCLK 180
 Db 122 GYIPLSKFPNKLKNYCNPDRERLPWFTTDPKRMWLDIDPRCTTTPPSGGPYQCLK 181

Qy 181 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRTPENFCKNLBENYCRNPDKGRAPWHT 240
 Db 182 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRTPENFCKNLBENYCRNPDKGRAPWHT 241

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 242 TNSQVRWEYCKIPSCDSSPV 261

Qy 1 VYLSECKTGKNGNYRGTMSKTRGKTCOKWSSTSPPHRFRSPATHPSGLBENYCRNDN 60
 Db 1 DPOGPWCYTDPERKYDIDICRCRCHCSENYDGKISKMSGLECQAMDSOPRAH 60

Qy 61 DPOGPWCYTDPERKYDIDICRCRCHCSENYDGKISKMSGLECQAMDSOPRAH 120

Db 121 GYIPLSKFPNKLKNYCNPDRERLPWFTTDPKRMWLDIDPRCTTTPPSGGPYQCLK 180
 Qy 181 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRTPENFCKNLBENYCRNPDKGRAPWHT 240
 Db 181 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRTPENFCKNLBENYCRNPDKGRAPWHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 241 TNSQVRWEYCKIPSCDSSPV 260

Query Match 99.7%; Score 1535; DB 2; Length 374;
 Best Local Similarity 99.6%; Pred. No. 1.6e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: January 25, 2006, 17:11:54
 Job time : 46 SECs

RESULT 15
 US-09-377-250-2
 ; Sequence 2, Application US/09377250
 ; Patent No. 6365364
 ; GENERAL INFORMATION:
 ; APPLICANT: MANN, KENNETH G.
 ; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
 ; FILE REFERENCE: 48409360
 ; CURRENT APPLICATION NUMBER: US/09/377, 250
 ; CURRENT FILING DATE: 1999-08-19
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: angiogenesis inhibitor
 ; FEATURE:

Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC syndrome, myocardial angiogenesis, plaque neovascularisation,
 CC telangiectasia, haemophilic joints, angiobronia and wound granulation.

CC As a centrifugation technique is not employed in the process, damage to
 CC the cells with concomitant release of undesirable biological materials
 CC such as cytochromes, pigments, enzymes, chemicals and other undesirable
 CC cellular constituents and debris, is prevented. Large scale recovery and
 CC purification of proteins is greater than that obtained from prior art
 CC methods. Active Angiostatin can be stored in buffers for extended periods
 CC of time, in vials or other containers, either in solution which may be
 CC liquid or frozen, or lyophilised

QY 1 VYLSECKTGKNGKRYGTMSTKNGTICRKWMSSTSPHRPRSPATHPSEGLENCRNPDN 60
 CC

Db 1 VYLSECKTGKNGKRYGTMSTKNGTICRKWMSSTSPHRPRSPATHPSEGLENCRNPDN 60
 CC

QY 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

Db 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

QY 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

Db 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

QY 181 GTGENYRGNVAVTVSGHTCQHMSAQTPHTERTPENFPCNLDENYCRNPDGKAPWHT 240
 CC

Db 181 GTGENYRGNVAVTVSGHTCQHMSAQTPHTERTPENFPCNLDENYCRNPDGKAPWHT 240
 CC

QY 241 TNSQVRWEVCKLIPSCDSSPV 260
 CC

Db 241 TNSQVRWEVCKLIPSCDSSPV 260
 CC

RESULT 2

AAU01209
 ID AAU01209 standard; protein: 260 AA.
 XX
 AC AAU01209;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DB Human Angiostatin (hAsv3) protein.
 XX
 KW Human; Angiostatin; recombinant production; cation exchange column;
 KW fermentation; angiogenesis mediated disease; leukaemia; tumour;
 KW rheumatoid arthritis; plaque neovascularisation.
 XX
 OS Homo sapiens.
 XX
 PN WO200140260-A2.
 XX
 PD 07-JUN-2001.
 XX
 PP 04-DEC-2000; 2000WO-US032843.
 XX
 PR 03-DEC-1999; 99US--0168919P.
 XX
 PA (ENTR-) ENTREMED INC.
 XX
 PI Medsen J, Liang H, Sim KL, Zhou X, Chang-Murad A, Boerner RJ;
 PI Bermejo JL, Mistri FR, Schrimsher JL, Shepard SR;
 XX
 DR WPI; 2001-408277/43.
 DR N-PSDB; AAS04181.

Purifying recombinant angiostatin, involves applying fermented broth containing angiostatin to expanded bed cation exchange column, anion exchange column, hydroxyapatite column, hydrophobic column and a membrane.

Example 1: Page 22; 49pp; English.

The present sequence representing Angiostatin protein is given in an invention providing a method for recombinant production, recovery and purification of angiostatin protein. Purification of recombinant angiostatin comprises applying crude fermentation broth containing the protein to an expanded bed cation exchange column, eluting it, and applying the eluate to anion exchange column, repeating the process of eluting and applying, to hydroxyapatite column, hydrophobic column and membrane, in order, and collecting fluid passing through the membrane. Angiostatin is useful for treating angiogenesis mediated diseases, including solid tumours, leukaemia, tumour metastases, benign tumours, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, Osler-Webber

CC

QY 1 VYLSECKTGKNGKRYGTMSTKNGTICRKWMSSTSPHRPRSPATHPSEGLENCRNPDN 60
 CC

Db 1 VYLSECKTGKNGKRYGTMSTKNGTICRKWMSSTSPHRPRSPATHPSEGLENCRNPDN 60
 CC

QY 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

Db 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

QY 1 VYLSECKTGKNGKRYGTMSTKNGTICRKWMSSTSPHRPRSPATHPSEGLENCRNPDN 60
 CC

Db 1 VYLSECKTGKNGKRYGTMSTKNGTICRKWMSSTSPHRPRSPATHPSEGLENCRNPDN 60
 CC

QY 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

Db 61 DPGPWCYTDPERKYDCLRCERCBMCSGENYDGKISKTMGSLCOWDSOPHAH 120
 CC

QY 121 GYIPSKEPNKLKKNYCNPDRSLRPFCFTDPNKRWECDIPRCTTPPPSSGPYQCLK 180
 CC

Db 121 GYIPSKEPNKLKKNYCNPDRSLRPFCFTDPNKRWECDIPRCTTPPPSSGPYQCLK 180
 CC

QY 181 GTGENYRGNVAVTVSGHTCQHMSAQTPHTERTPENFPCNLDENYCRNPDGKAPWHT 240
 CC

Db 181 GTGENYRGNVAVTVSGHTCQHMSAQTPHTERTPENFPCNLDENYCRNPDGKAPWHT 240
 CC

QY 241 TNSQVRWEVCKLIPSCDSSPV 260
 CC

Db 241 TNSQVRWEVCKLIPSCDSSPV 260
 CC

RESULT 3

ADK40316
 ID ADK40316 standard; protein: 869 AA.
 XX
 AC ADK40316;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DR C-terminal albumin-angiostatin fusion protein.
 XX
 KW cytotoxic; vaccine; albumin fusion protein; angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer; collagen.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003066085-A1.
 XX
 PD 14-AUG-2003.
 XX
 PP 07-FEB-2003; 2003WO-IB000433.
 XX
 PR 07-FEB-2002; 2002US-0355547P.
 XX
 PA (AVET) AVENTIS BEHRING GMBH.
 PA (DELB) DELTA BIOTECHNOLOGY LTD.
 XX
 PI Martini P, Celik I, Kisker O, Sleep D, Ray J, Hauser H;
 XX
 DR WPI; 2003-731479/69.
 DR N-PSDB; ADK40315.
 XX
 PT New albumin fusion protein comprising an angiogenesis inhibiting peptide and an albumin having an albumin activity, or their fragments or

PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
 XX
 PS Disclosure; Fig 8; 136pp; English.
 XX
 CC The invention relates to an albumin fusion protein comprising an
 CC angiogenesis inhibiting peptide and an albumin having an albumin
 activity, or their fragments or variants. The albumin fusion proteins,
 CC compositions, vaccines and methods are useful for treating angiogenesis-
 dependent tumor, e.g. cancer. This sequence represents an C-terminal
 CC albumin-angiostatin fusion protein.
 XX
 SQ Sequence 869 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.8%	7	869
Matches	259;	Conservative	1;
Mismatches	0;	Indels	0;
Gaps	0;		

QY 1 VYLSECKTGNGKNGNYRGTMSKTKNGTICKQKWSSTSPhRPRSPATHPSSEGLENVCRNPDN 60
 Db 610 VYLSECKTGNGKNGNYRGTMSKTKNGTICKQKWSSTSPhRPRSPATHPSSEGLENVCRNPDN 669
 QY 61 DPGQWCTTDPEKRYCDILECEBECRMECSGENYDGKISKTMGULECQAWDSOPHAK 120
 Db 670 DPGQWCTTDPEKRYCDILECEBECRMECSGENYDGKISKTMGULECQAWDSOPHAK 729
 QY 121 GYIPSKFPNKNLKKYCRNDRFLPWFCTDPNKRWECLDIPRCTTPSSGPTVCLK 180
 Db 730 GYIPSKFPNKNLKKYCRNDRFLPWFCTDPNKRWECLDIPRCTTPSSGPTVCLK 789
 QY 181 GTGENYRGNVAVTVSGHTCQHWAQOPTPHTRTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 Db 790 GTGENYRGNVAVTVSGHTCQHWAQOPTPHTRTPENFPCKLNDENYCRNPDGKRAPWCHT 849
 QY 241 TNSQRWEYCKIPSCDSPPV 260
 Db 850 TNSQRWEYCKIPSCDSPPV 869

RESULT 4

ADK40314
 ID ADK40314 standard; protein; 869 AA.
 AC
 XX
 AC
 XX
 DT 06-MAY-2004 (first entry)
 DB N-terminal angiostatin-albumin fusion protein.
 XX
 KW cytostatic; vaccine; albumin fusion protein;
 KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003066085-A1.

RESULT 5

AGT9748
 ID AAG79748 standard; protein; 260 AA.
 AC
 XX
 AC
 XX
 DT 18-MAR-2003 (first entry)
 DB Human plasminogen kringle domains 1-3, K1-3.
 XX
 KW Human; plasminogen; angiostatin; neovascularisation; kringle domain;
 KW cell proliferation; viral vector; replication-defective; cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200288173-A2.
 XX
 PD 07-NOV-2002.
 XX
 PR 14-AUG-2003.
 XX
 PR 07-FEB-2003; 2003WO-IB000433.
 XX
 PR 07-FEB-2002; 2002US-0355547P.
 PR 05-APR-2002; 2002US-0370634P.
 XX
 PA (AVET) AVENTIS BEHRING GMBH.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX
 PT Mertins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
 XX
 DR WPI; 2003-731479/69.
 DR N-PSDB; ADK40313.
 PT New albumin fusion protein comprising an angiogenesis inhibiting peptide
 PT and an albumin having an albumin activity, or their fragments or
 PT XX
 PS Sequence 869 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.8%	7	869
Matches	259;	Conservative	1;
Mismatches	0;	Indels	0;
Gaps	0;		

QY 1 VYLSECKTGNGKNGNYRGTMSKTKNGTICKQKWSSTSPhRPRSPATHPSSEGLENVCRNPDN 60
 Db 25 VYLSECKTGNGKNGNYRGTMSKTKNGTICKQKWSSTSPhRPRSPATHPSSEGLENVCRNPDN 84
 QY 61 DPGQWCTTDPEKRYCDILECEBECRMECSGENYDGKISKTMGULECQAWDSOPHAK 120
 Db 85 DPGQWCTTDPEKRYCDILECEBECRMECSGENYDGKISKTMGULECQAWDSOPHAK 144
 QY 121 GYIPSKFPNKNLKKYCRNDRFLPWFCTDPNKRWECLDIPRCTTPSSGPTVCLK 180
 Db 145 GYIPSKFPNKNLKKYCRNDRFLPWFCTDPNKRWECLDIPRCTTPSSGPTVCLK 204
 QY 181 GTGENYRGNVAVTVSGHTCQHWAQOPTPHTRTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 Db 205 GTGENYRGNVAVTVSGHTCQHWAQOPTPHTRTPENFPCKLNDENYCRNPDGKRAPWCHT 264
 QY 241 TNSQRWEYCKIPSCDSPPV 260
 Db 265 TNSQRWEYCKIPSCDSPPV 284

PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
 XX
 PS Disclosure; Fig 6; 136pp; English.
 XX
 CC The invention relates to an albumin fusion protein comprising an
 CC angiogenesis inhibiting peptide and an albumin having an albumin
 activity, or their fragments or variants. The albumin fusion proteins,
 CC compositions, vaccines and methods are useful for treating angiogenesis-
 dependent tumor, e.g. cancer. This sequence represents an N-terminal
 CC angiostatin-albumin fusion protein.
 XX
 SQ Sequence 869 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.8%	7	869
Matches	259;	Conservative	1;
Mismatches	0;	Indels	0;
Gaps	0;		

QY 1 VYLSECKTGNGKNGNYRGTMSKTKNGTICKQKWSSTSPhRPRSPATHPSSEGLENVCRNPDN 60
 Db 25 VYLSECKTGNGKNGNYRGTMSKTKNGTICKQKWSSTSPhRPRSPATHPSSEGLENVCRNPDN 84
 QY 61 DPGQWCTTDPEKRYCDILECEBECRMECSGENYDGKISKTMGULECQAWDSOPHAK 120
 Db 85 DPGQWCTTDPEKRYCDILECEBECRMECSGENYDGKISKTMGULECQAWDSOPHAK 144
 QY 121 GYIPSKFPNKNLKKYCRNDRFLPWFCTDPNKRWECLDIPRCTTPSSGPTVCLK 180
 Db 145 GYIPSKFPNKNLKKYCRNDRFLPWFCTDPNKRWECLDIPRCTTPSSGPTVCLK 204
 QY 181 GTGENYRGNVAVTVSGHTCQHWAQOPTPHTRTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 Db 205 GTGENYRGNVAVTVSGHTCQHWAQOPTPHTRTPENFPCKLNDENYCRNPDGKRAPWCHT 264
 QY 241 TNSQRWEYCKIPSCDSPPV 260
 Db 265 TNSQRWEYCKIPSCDSPPV 284

XX

This sequence represents kringle domains 1-3 of human plasminogen. A 38 KD N-terminal fragment of plasminogen is referred to as angiostatin and inhibits neovascularisation.

CC

the parent molecule. However, angiostatin containing all 4 kringle domains (K1-4) was found to be no more potent as an inhibitor of cell

CC

proliferation than an angiostatin only containing K1-3. Therefore,

CC

kringle 4 does not possess inhibitory activity. A fragment of the

CC

plasminogen coding sequence may be used in the recombinant viral vector of the invention for obtaining angiostatin activity.

CC

The vector comprises a promoter capable of expressing human angiostatin operably linked to a

CC

structural gene encoding one or more domains of human angiostatin. The vector, which may be a replication-defective viral vector, is useful for

CC

inhibiting angiogenesis in a mammal, especially with cancer or a tumor

SQ

Sequence 260 AA;

Query Match

99.7%; Score 1535; DB 6; Length 260;

Best Local Similarity

99.6%; Pred. No. 2.1e-90;

Matches

259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy

1 VYLSECKTGNGKNYKGRTGMSKTKNGITCQKWSSTSFRPRSPATHSEGLENYCRNPDN

Db

1 VYLSECKTGNGKNYKGRTGMSKTKNGITCQKWSSTSFRPRSPATHSEGLENYCRNPDN 60

Oy

61 DPGGPWCTTDPERKRYCDILRCERCECMHSEGENTDGKISITMSGLECOAWDSOPHAH 120

Db

61 DPGGPWCTTDPERKRYCDILRCERCECMHSEGENTDGKISITMSGLECOAWDSOPHAH 120

Oy

121 GTIPSKPNKLKKYCRNDRPDRPCTTPNPKMELCDIPRCTTPPSGSPTYQCLK 180

Db

121 GTIPSKPNKLKKYCRNDRPDRPCTTPNPKMELCDIPRCTTPPSGSPTYQCLK 180

Oy

181 GTGENYRGNVAVTVSGHTCQHNSAQPTPHTERTPENFFCKNLDENYCRNPDGKRAPWHT 240

Db

181 GTGENYRGNVAVTVSGHTCQHNSAQPTPHTERTPENFFCKNLDENYCRNPDGKRAPWHT 240

Oy

241 TNSQVREYCKLIPSCDSSPV 260

Db

241 TNSQVREYCKLIPSCDSSPV 260

RESULT 6

AY02109

ID

AY02109 standard; protein; 268 AA.

AC

AY02109;

XX

16-JUL-1999 (first entry)

DT

A multifunctional protein of the invention.

DE

XX Angiostatin; endostatin; interferon; thrombospondin; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis; tumor cell production.

XX

Synthetic.

OS

Homo sapiens.

XX

WO9916889-A1.

PR

01-OCT-1997; 97US-0060609P.

XX

(SEAR) SEARLE & CO G D.

PA

Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;

PI

McKearn JP;

XX

WPI; 1999-255098/21.

DR

New multifunctional proteins useful for treating angiogenic-mediated diseases.

XX

The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties.

CC

The protein can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.

CC

They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the invention.

XX

Sequence 268 AA;

Query Match

99.7%; Score 1535; DB 2; Length 268;

Best Local Similarity

99.6%; Pred. No. 2.2e-90;

Matches

259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy

1 VYLSECKTGNGKNYKGRTGMSKTKNGITCQKWSSTSFRPRSPATHSEGLENYCRNPDN

Db

1 VYLSECKTGNGKNYKGRTGMSKTKNGITCQKWSSTSFRPRSPATHSEGLENYCRNPDN 62

Oy

61 DPGGPWCTTDPERKRYCDILRCERCECMHSEGENTDGKISITMSGLECOAWDSOPHAH 120

Db

61 DPGGPWCTTDPERKRYCDILRCERCECMHSEGENTDGKISITMSGLECOAWDSOPHAH 120

Oy

121 GTIPSKPNKLKKYCRNDRPDRPCTTPNPKMELCDIPRCTTPPSGSPTYQCLK 180

Db

121 GTIPSKPNKLKKYCRNDRPDRPCTTPNPKMELCDIPRCTTPPSGSPTYQCLK 180

Oy

181 GTGENYRGNVAVTVSGHTCQHNSAQPTPHTERTPENFFCKNLDENYCRNPDGKRAPWHT 240

Db

181 GTGENYRGNVAVTVSGHTCQHNSAQPTPHTERTPENFFCKNLDENYCRNPDGKRAPWHT 240

Oy

241 TNSQVREYCKLIPSCDSSPV 260

Db

241 TNSQVREYCKLIPSCDSSPV 260

RESULT 7

AY02102

ID

AY02102 standard; protein; 285 AA.

AC

AY02102;

XX

16-JUL-1999 (first entry)

DT

A multifunctional protein of the invention.

DE

XX Angiostatin; endostatin; interferon; thrombospondin; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis; tumor cell production.

XX

Synthetic.

OS

Homo sapiens.

XX

WO9916889-A1.

PR

08-APR-1999.

XX

Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;

PI

McKearn JP;

PF 30-SEP-1998; 98WO-US020464.
 XX PR 01-OCT-1997; 97US-0060609P.
 XX PA (SEAR) SEARLE & CO G D.
 XX PI Bolanowski MA, Caparon MH, Casperson GP, Gregory SA, Klein BK;
 XX DR WPI; 1999-255098/21.
 XX PT New multifunctional proteins useful for treating angiogenic-mediated
 PT diseases.
 XX PS Claim 5; Page 97-98; 121pp; English.

XX CC The specification describes multifunctional proteins which comprise
 CC combinations of angiostatin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have anti-
 CC angiogenic and/or anti-tumor activity. The multifunctional protein may
 CC exhibit useful properties such as having similar or greater biological
 CC activity when compared to a single factor or by having improved half-life
 CC or decreased adverse side effects, or a combination of these properties.
 CC The proteins can be used for treating an angiogenic-mediated disease,
 CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.
 CC They can also be used for inhibiting the production of tumor cells
 CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
 CC colon, renal, bladder cancers, melanoma, hepatoma, sarcoma and lymphoma)
 CC in a patient and for inhibiting tumor growth. The present Sequence
 XX represents a multifunctional protein of the invention.

XX SQ Sequence 285 AA;

Query Match	99.7%	Score 1535;	DB 2;	Length 285;
Best Local Similarity	99.6%	Pred. No.	2.3e-90;	
Matches	259;	Conservative	0;	Mismatches
			1;	Indels
			0;	Gaps
			0;	

QY 1 VYLSECKTGKNGKNYRGTMKTKNGITCOKNSSTSPPRPRSPATHSEGLENCRNPDN 60
 Db 2 VYLSECKTGKNGKNYRGTMKTKNGITCOKNSSTSPPRPRSPATHSEGLENCRNPDN 79
 QY 61 DPOGFWCYTIDPEKRYDYCILCEBECBECMHSGENYDGKISKTMMSGLECAWDSOPHAH 120
 Db 80 DPOGFWCYTIDPEKRYDYCILCEBECBECMHSGENYDGKISKTMMSGLECAWDSOPHAH 139
 QY 121 GYIPSKEPKPNLKKNYCRNDRELAPWCFTIDPNKGWELCDIPRCTTPSSGPYQICK 180
 Db 140 GYIPSKEPKPNLKKNYCRNDRELAPWCFTIDPNKGWELCDIPRCTTPSSGPYQICK 199
 QY 121 GYIPSKEPKPNLKKNYCRNDRELAPWCFTIDPNKGWELCDIPRCTTPSSGPYQICK 180
 Db 121 GYIPSKEPKPNLKKNYCRNDRELAPWCFTIDPNKGWELCDIPRCTTPSSGPYQICK 180
 QY 181 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRPENFPCNLDENYCRNPDGKRAPWCHT 240
 Db 200 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRPENFPCNLDENYCRNPDGKRAPWCHT 259
 QY 241 TNSQRWEYCKIPSCDSSPV 260
 Db 260 TNSQRWEYCKIPSCDSSPV 279

RESULT 8

AAR33961 ID AAR33961 standard; protein; 339 AA.

AC AC AAR33961;
 XX DT 10-MAR-1996 (first entry)

XX DE Human plasminogen peptide fragment.

XX KW Angiotatin; plasminogen; endothelial inhibitor; therapeutic; gene therapy.

XX OS Homo sapiens.

XX PN WO9529242-A1.
 XX PR 02-NOV-1995.
 XX PA 26-APR-1995; 95WO-US005107.
 XX PR 26-APR-1994; 94US-00348629.
 XX PR 20-OCT-1994; 94US-00326785.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PT O'reilly MS, Polkman MJ, Sim KL, Cao Y;
 XX DR WPI; 1995-382990/49.
 XX PR Endothelial inhibitor Angiostatin - useful to treat angiogenic mediated
 PT disease esp. angiogenesis and cancer.

XX PS Claim 4; Page 81-82; 108pp; English.

XX CC The sequence represents a plasminogen fragment which is compared with the
 CC corresponding plasminogen fragments of monkey (AAR8362), Pig (AAR83963)
 CC and cattle (AAR83961) origin (in Fig.2), as well as the with the first
 CC 339 amino acids of mouse angiostatin (AAR83960) (i.e. aa's 98-436 of the
 CC complete 812 aa plasminogen molecule AAR83959). Human angiostatin is a
 CC plasminogen fragment starting at aa 97 or 99 of the complete plasminogen
 CC molecule. Angiostatin is an endothelial inhibitor, which reversibly
 CC inhibits proliferation of endothelial cells and thereby inhibits
 CC angiogenesis. It is useful in the treatment of a human or animal with
 CC angiogenesis mediated disease e.g. arthritis, macular degeneration,
 CC diabetic retinopathy or cancer. Cells comprising angiostatin-coding
 CC sequences are useful for gene therapy of primary tumors

XX SQ Sequence 339 AA;

Query Match	99.7%	Score 1535;	DB 2;	Length 339;
Best Local Similarity	99.6%	Pred. No.	2.7e-90;	
Matches	259;	Conservative	0;	Mismatches
			1;	Indels
			0;	Gaps
			0;	

QY 1 VYLSECKTGKNGKNYRGTMKTKNGITCOKNSSTSPPRPRSPATHSEGLENCRNPDN 60
 Db 2 VYLSECKTGKNGKNYRGTMKTKNGITCOKNSSTSPPRPRSPATHSEGLENCRNPDN 60
 QY 61 DPOGFWCYTIDPEKRYDYCILCEBECBECMHSGENYDGKISKTMMSGLECAWDSOPHAH 120
 Db 61 DPOGFWCYTIDPEKRYDYCILCEBECBECMHSGENYDGKISKTMMSGLECAWDSOPHAH 120
 QY 121 GYIPSKEPKPNLKKNYCRNDRELAPWCFTIDPNKGWELCDIPRCTTPSSGPYQICK 180
 Db 121 GYIPSKEPKPNLKKNYCRNDRELAPWCFTIDPNKGWELCDIPRCTTPSSGPYQICK 180
 QY 181 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRPENFPCNLDENYCRNPDGKRAPWCHT 240
 Db 200 GTGENYRGNVAVTSGHTCQHWAQOPTPHTRPENFPCNLDENYCRNPDGKRAPWCHT 240
 QY 241 TNSQRWEYCKIPSCDSSPV 260
 Db 241 TNSQRWEYCKIPSCDSSPV 260

OS Homo sapiens.
 XX
 PN WO9635774-A2.
 XX
 PD 14-NOV-1996.
 XX
 PR 26-APR-1995; 96WO-US005856.
 PR 22-FEB-1996; 96US-00625598.
 PR 08-MAR-1996; 96US-00612788.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Folkman MJ, O'reilly MS, Cao Y, Sim KH, Lin J;
 XX
 DR WPI; 1996-5118662/51.

PT Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy.

PS Claim 59; Page 96-97; 203pp; English.

CC The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4BKUS protein. The aggregate angiostatin has a Mol. Wt. of 45-65 kd and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine Plasminogen. The active component can be used for treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy. The present sequence, which is the N-terminal fragment of human angiostatin, is a specific aggregate angiostatin which can be used in the invention

Sequence 339 AA;

Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 2.7e-90; 1; Indels 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1;

QY 1 VYLSECKTGNGKNGRTGMSKTKNGITCQKMSSTSPPHRPRESATHSERGLEENYCRNPDN 60
 Db 1 VYLSECKTGNGKNGRTGMSKTKNGITCQKMSSTSPPHRPRESATHSERGLEENYCRNPDN 60
 QY 61 DROGPWCYTDDPEKRYDCDILCECBECRCPHMSGGENTDGKISKTMGLEQAWDSOPHAH 120
 Db 61 DFOGPWCYTDDPEKRYDCDILCECBECRCPHMSGGENTDGKISKTMGLEQAWDSOPHAH 120
 QY 121 GYPSKPKPNKLNKKNYCRNPDKBLRPWCFTDPNPKWELCIPRCCTTPSSGGPTYQCLK 180
 Db 121 GYPSKPKPNKLNKKNYCRNPDKBLRPWCFTDPNPKWELCIPRCCTTPSSGGPTYQCLK 180
 QY 181 GTCGTYKGNVAVTUSGHTCQHSAQTPTHTPPTPENPKCQKLDENYCRNPDKRAPWHT 240
 Db 181 GTCGTYKGNVAVTUSGHTCQHSAQTPTHTPPTPENPKCQKLDENYCRNPDKRAPWHT 240
 QY 241 TNSQVRWYCKLIPSCDSSPV 260
 Db 241 TNSQVRWYCKLIPSCDSSPV 260

PS Example 27; Fig 2A-C; 165pp; English.

XX The invention relates to inhibition of endothelial cell proliferation that comprises administering to an endothelial cell a plasminogen fragment having an amino acid sequence similar to the kringle 1-5 region of a plasminogen molecule. The plasminogen fragments can be derived from murine, human, Rhesus, porcine or bovine plasminogens. The plasminogen fragments can be used for modulating angiogenesis and treating angiogenic disease e.g. solid tumours; for treating excessive or abnormal stimulation of endothelial cells; as a birth control agent; and in the treatment of disease that have angiogenesis as a pathological consequence (see AW94036 for details on the various diseases the plasminogen fragments can be used to treat). The nucleotide sequences encoding the plasminogen fragments can also be used for gene therapy. The products can be used for the production of antibodies and in detection and diagnosis. Sequences AW94037 to W401 represent angiostatin fragments (protein derivatives of angiostatin or plasminogen, having an endothelial cell proliferation activity) of murine, human, Rhesus, porcine and bovine angiostatins respectively. The kringle regions that can be used in the invention are indicated in the features

Sequence 339 AA;

Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 2.7e-90; 1; Indels 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1;

QY 1 VYLSECKTGNGKNGRTGMSKTKNGITCQKMSSTSPPHRPRESATHSERGLEENYCRNPDN 60
 Db 1 VYLSECKTGNGKNGRTGMSKTKNGITCQKMSSTSPPHRPRESATHSERGLEENYCRNPDN 60

RESULT 10
 AAW94038
 ID AAW94038 standard; protein; 339 AA.
 XX
 AC AAW94038;
 XX

QY 61 DROGPWCYTDPBKRYCQDIRCEECMHCSGENYQKISKTMMSGLEQWDSOPHAI 120
 XX PS Example 27; Fig 2A-C; 70bp; English.
 Db 61 DROGPWCYTDPBKRYCQDIRCEECMHCSGENYQKISKTMMSGLEQWDSOPHAI 120
 QY 121 GYPSKPKNKLNKGNYCRNPDRBLRPNPCFTTDPKRNLCDIPRCTTPPSGGPTYCLK 180
 Db 121 GYPSKPKNKLNKGNYCRNPDRBLRPNPCFTTDPKRNLCDIPRCTTPPSGGPTYCLK 180
 QY 181 GTGENTRGNVAVTWSGHTCOHWSAQTPTHERTPENPKDIDENTYCRNPGKRAPWHT 240
 Db 181 GTGENTRGNVAVTWSGHTCOHWSAQTPTHERTPENPKDIDENTYCRNPGKRAPWHT 240
 QY 241 TNSQVRWEYCKIPSCDSPPV 260
 Db 241 TNSQVRWEYCKIPSCDSPPV 260

RESULT 11

AAM5018
 ID AAM5018 standard; protein; 339 AA.
 XX
 AC AAM5018;
 XX
 DT 12-MAR-2002 (first entry)

DB Human angiostatin.

XX

Angiostatin; plasminogen; human; angiogenesis; endothelial cell; cell proliferation; inhibitor; tumour; antisporotic; cytosstatic; vasotropic; antitumour; dermatological; antiinflammatory; antidiabetic; antibacterial; antiatherosclerotic; gynaecological; antipyretic; cardiotonic; contraceptive; therapy.

XX Homo sapiens.

XX

Key Location/Qualifiers

PT Region 6..255 /label= Kringle-1-3
 PT Region 6..165 /label= Kringle-1-2
 PT Region 6..84 /label= Kringle-1
 PT Region 88..255 /label= Kringle-2-3
 PT Region 88..165 /label= Kringle-2
 PT Region 178..255 /label= Kringle-3

Query Match 99.7%; Score 1535; DB 4; Length 339; Best Local Similarity 99.6%; Pred. No. 2; te=90; Matches 259; Conservative 0; Mismatches 1; Index 0; Gaps 0; Matches 1 VILSECKTGNGKNGYRGTMKTKGTRQKWSSTSPPRPFSPATHPSBGLERNYCRNPDN 60
 Db 1 VILSECKTGNGKNGYRGTMKTKGTRQKWSSTSPPRPFSPATHPSBGLERNYCRNPDN 60
 QY 61 DROGPWCYTDPBKRYCQDIRCEECMHCSGENYQKISKTMMSGLEQWDSOPHAI 120
 Db 61 DROGPWCYTDPBKRYCQDIRCEECMHCSGENYQKISKTMMSGLEQWDSOPHAI 120
 QY 121 GYPSKPKNKLNKGNYCRNPDRBLRPNPCFTTDPKRNLCDIPRCTTPPSGGPTYCLK 180
 Db 121 GYPSKPKNKLNKGNYCRNPDRBLRPNPCFTTDPKRNLCDIPRCTTPPSGGPTYCLK 180
 QY 181 GTGENTRGNVAVTWSGHTCOHWSAQTPTHERTPENPKDIDENTYCRNPGKRAPWHT 240
 Db 181 GTGENTRGNVAVTWSGHTCOHWSAQTPTHERTPENPKDIDENTYCRNPGKRAPWHT 240
 QY 241 TNSQVRWEYCKIPSCDSPPV 260
 Db 241 TNSQVRWEYCKIPSCDSPPV 260

RESULT 12

ADG47024
 ID ADG47024 standard; protein; 339 AA.
 XX
 AC ADG47024;
 XX
 DT 11-MAR-2004 (first entry)

DB Human angiostatin protein.

XX

DR Human angiostatin protein.

XX

Angiostatin; cell proliferation; angiogenic-mediated disease; cancer; arthritis; macular degeneration; diabetic retinopathy; psoriasis; scleroderma; Crohn's disease; wound; peptic ulcer; fracture; gene therapy; plasminogen; cyrotactic; ophthalmological; dermatological; antiinflammatory; vulnerability; human.

XX

WPI; 2001-647990/74.

XX Inhibiting endothelial cell proliferation, useful for treating angiogenic diseases such as cancer, arthritis, comprises administering a plasminogen fragment corresponding to kringle structures of plasminogen molecule.

Db 1 VYLSECKTGNGSKNYRGTMSKTKNGTICKQKNSSTSPPRPRSPATPSBGLENYCRNPDN 60
 CC degeneration, corneal graft rejection, neovascular glaucoma, retrothalal
 Db 61 DPGQPCYTTDPBKRYCDILCECBMCHGENTDGKSKTMSSGLECQWDSDSPHAH 120
 CC fibroplasia, rubrosis and Osler-Weber syndrome; myocardial angiogenesis,
 QY 61 DPGQPCYTTDPBKRYCDILCECBMCHGENTDGKSKTMSSGLECQWDSDSPHAH 120
 CC plaque neovascularisation, telangiectasia, haemophilic joints;
 Db 121 GYIPSKPKNKLUKKNYCRNPDRBLRPWCPTTDPNKREWLCIDIPRCTTPRSSGPTVCLK 180
 CC angiofibroma, wound granulation, and excessive or abnormal stimulation of
 QY 121 GYIPSKPKNKLUKKNYCRNPDRBLRPWCPTTDPNKREWLCIDIPRCTTPRSSGPTVCLK 180
 CC endothelial cells, intestinal cells, atherosclerosis, sclerodermal and
 Db 121 GYIPSKPKNKLUKKNYCRNPDRBLRPWCPTTDPNKREWLCIDIPRCTTPRSSGPTVCLK 180
 CC hypertrophic scars, keloid scars. The DNA constructs may be used in the
 QY 181 GTGENTRGNVAVTVSHTCQWMSAQTPHTHRTTPENPKNDENYCRNPDGKRAPWHT 240
 CC gene therapy. The present sequence is a human angiostatin used in the
 Db 181 GTGENTRGNVAVTVSHTCQWMSAQTPHTHRTTPENPKNDENYCRNPDGKRAPWHT 240
 CC construction of immunofusion containing human immunoglobulin gamma (IgG)
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 CC FC fragment
 Db 241 TNSQVRWEYCKIPSCDSSPV 260
 XX Sequence 363 AA:
 RESULT 14
 AAY70255 Standard; protein: 363 AA.
 ID AAY70255; Matches 259; Best Local Similarity 99.6%; Score 1537; Length 363;
 AC AAY70255; DT 06-JUN-2000 (first entry)
 XX Human angiogenesis inhibitor, angiostatin.
 DE Human angiogenesis inhibitor, angiostatin.
 KW Human; immunoglobulin gamma Fc fragment; angiostatin; immunofusin;
 KW angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic;
 KW antiangiogenic; anti-diabetic; ophthalmological; immunosuppressant;
 KW vasoconstrictor; vulnerary; treatment; antiarteriosclerosis; tumour;
 KW metastasis; atherosclerosis; phoriasis; rheumatoid arthritis;
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
 KW wound granulation; keloid scar; gene therapy.
 OS Homo sapiens.
 XX WO200011033-A2.
 PN 02-MAR-2000.
 XX 25-AUG-1999; 99WO-US019329.
 PR 25-AUG-1998; 98US-009783P.
 PA (LEXI-) LEXINGEN PHARM CORP.
 PI LO K, Li Y, Gillies SD;
 XX WPI: 2000-237615/20.
 DR N-PSDB; AA251295.
 XX Novel fusion protein of angiostatin or endostatin and an immunoglobulin
 PT region, useful for treating conditions mediated by angiogenesis, such
 PT as rheumatoid arthritis, tumors and macular degeneration.
 XX Example 4; Page 45-46; 68PP; English.

The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including haemangiomas, acoustic neuromas, neurofibromas, trichoblastoma and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular

Query Match 99.7%; Score 1537; DB 3; Length 363;
 Best Local Similarity 99.6%; Pred. No. 2.9e-90; Mismatches 0; Indels 0; Gaps 0;
 Matches 259; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Db 1 VYLSECKTGNGSKNYRGTMSKTKNGTICKQKNSSTSPPRPRSPATPSBGLENYCRNPDN 60
 QY 1 VYLSECKTGNGSKNYRGTMSKTKNGTICKQKNSSTSPPRPRSPATPSBGLENYCRNPDN 60
 Db 2 VYLSECKTGNGSKNYRGTMSKTKNGTICKQKNSSTSPPRPRSPATPSBGLENYCRNPDN 60
 QY 61 DPGQPCYTTDPBKRYCDILCECBMCHGENTDGKSKTMSSGLECQWDSDSPHAH 120
 Db 62 DPGQPCYTTDPBKRYCDILCECBMCHGENTDGKSKTMSSGLECQWDSDSPHAH 120
 QY 121 GYIPSKPKNKLUKKNYCRNPDRBLRPWCPTTDPNKREWLCIDIPRCTTPRSSGPTVCLK 180
 Db 122 GYIPSKPKNKLUKKNYCRNPDRBLRPWCPTTDPNKREWLCIDIPRCTTPRSSGPTVCLK 180
 QY 181 GTGENTRGNVAVTVSHTCQWMSAQTPHTHRTTPENPKNDENYCRNPDGKRAPWHT 240
 Db 182 GTGENTRGNVAVTVSHTCQWMSAQTPHTHRTTPENPKNDENYCRNPDGKRAPWHT 240
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 242 TNSQVRWEYCKIPSCDSSPV 261
 XX Sequence 363 AA:
 RESULT 15
 AAY02106 Standard; protein: 364 AA.
 ID AAY02106; Matches 259; Best Local Similarity 99.6%; Score 1537; Length 363;
 XX AAY02106; DT 16-JUL-1999 (first entry)
 XX A multifunctional protein of the invention.
 DE Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; tumor cell production.
 KW KW KW KW KW
 OS Synthetic.
 OS Homo sapiens.
 XX WO9916889-A1.
 PN 01-OCT-1997; 97US-006069P.
 PD 08-APR-1999.
 XX PF 30-SEP-1999; 98WO-US025464.
 PR (SEAR) SEARLE & CO G D.
 PA Bolanoski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;
 PI Bolanoski JP;
 XX DR WPI; 1999-255098/21.
 XX PT New multifunctional proteins useful for treating angiogenic-mediated diseases.

xx
ps Claim 5; Page 101-102; 121pp; English.

xx
cc The specification describes multifunctional proteins which comprise
cc combinations of angiotatin, endosatin, interferon, thrombospondin,
cc intereron-inducible protein and platelet factor 4, and have anti-
angiogenic and/or anti-tumor activity. The multifunctional protein may
exhibit useful properties such as having similar or greater biological
activity when compared to a single factor or by having improved half-life.
cc or decreased adverse side effects, or a combination of these properties.
The proteins can be used for treating an angiogenic-mediated disease,
e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.
They can also be used for inhibiting the production of tumor cells
(characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)
cc in a patient and for inhibiting tumor growth. The present sequence
cc represents a multifunctional protein of the invention
xx

SQ Sequence 364 AA;

Query Match 99.7%; Score 1535; DB 2; Length 364;

Best Local Similarity 99.6%; Pred. No. 2.9e-90; Mismatches 0; Indels 0; Gaps 0;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VVLSCECKTGNGKNGYRGMSTKNGITOKWMSSTSPPRPRSPATHSEGLENYCNPDN 60

Db 3 VVLSCECKTGNGKNGYRGMSTKNGITOKWMSSTSPPRPRSPATHSEGLENYCNPDN 62

OY 61 DPGGPWCUTTDPEKRYDVGCDLUECBBGWAHCSGENYKGKISKTMGSLGACQMDSGPAH 120

Db 63 DPGGPWCUTTDPEKRYDVGCDLUECBBGWAHCSGENYKGKISKTMGSLGACQMDSGPAH 122

OY 121 GYTPSKFPNKLKNCYCNPDRSLRPNCFTTDPKRWECLDIPRCTTTPPSGGPTQCLK 180

Db 123 GYTPSKFPNKLKNCYCNPDRSLRPNCFTTDPKRWECLDIPRCTTTPPSGGPTQCLK 182

OY 181 GTGENYGNVAVTWSGHQCQHSAQTPTHTPENPCKNLIDENTCRNPGKRAWCHT 240

Db 183 GTGENYGNVAVTWSGHQCQHSAQTPTHTPENPCKNLIDENTCRNPGKRAWCHT 242

OY 241 TNSQVRMEYCKLPSCDSSPV 260

Db 243 TNSQVRMEYCKLPSCDSSPV 262

Search completed: January 25, 2006, 17:07:13
Job time : 138 secB

GenCore version 5.1.6
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OM Protein - protein search, using sw model

Run on: January 25, 2006, 17:02:00 ; Search time 39 Seconds
(without alignments)
641.445 Million cell updates/sec

Title: US-09-502-176-2
Perfect score: 1540
Sequence: I VYLSBCKTGNGKRYGTMISK. TNSQVRWYCKLPSCLSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1535	99.7	810	1
2	1442	93.6	810	2
3	1292	83.9	790	1
4	1291	83.8	812	1
5	1274	82.7	812	1
6	1237	80.3	810	2
7	881	57.2	2869	2
8	797	51.8	728	1
9	782	50.8	728	1
10	776.5	50.4	710	1
11	775	50.4	728	1
12	766.5	49.8	716	1
13	754.5	49.0	411	2
14	753.5	48.9	716	1
15	749	48.6	4548	1
16	739	48.0	711	1
17	739	48.0	A7136	
18	705	32.8	A12869	
19	499	32.4	455	2
20	391.5	25.4	A0332	
21	372	24.2	625	1
22	362.5	23.5	A0522	
23	357.5	23.2	AJ5827	
24	351	22.8	622	1
25	348	22.6	617	2
26	309.5	20.1	562	1
27	295.5	19.2	559	1
28	281	18.3	A29941	
29	18.1		B61545	

ALIGNMENTS

RESULT 1

PLRU

plasmin (EC 3.4.21-7) precursor [validated] - human
N;Contains: angiostatin; microplasmin; plasminogen

C;Species: Homo sapiens (man)

C;Accession: A5229; I52242; R26649; I62738; 184690; S93735; A00929; A04627; A04625; A0,

R;Petersen, T.F.; Martzen, M.R.; Ichinose, A.; Davie, E.W.

J. Biol. Chem. 265, 6104-6111, 1990

A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibr

A;Reference number: A35229; MUND:90202879; PMID:2318848

A;Accession: A35229

A;Molecule type: DNA

A;Residues: 1-810 <PTP>

A;Cross-references: UNIPROT:PO0747; UNIPROT:Q9UBQ9; UNIPROT:Q9UM12; UNIPARC:UPI000016AB

A;Experimental source: Leukocyte; lung fibroblast

R;Margaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Ti

Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990

A;Title: Definition of the transcription initiation site of human plasminogen gene in 1,

A;Reference number: 152242; MUND:91097523; PMID:2268308

A;Accession: 152242

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-16 <MAIL>

A;Cross-references: UNIPARC:UPI0000062A8; GB:M62890; NID:9190092; PIDN:AAA36454_1; PID

F;Forssgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.

FEBS Lett. 213, 254-260, 1987

A;Title: Molecular cloning and characterization of a full-length cDNA clone for human p

A;Reference number: A26646; MUND:87162490; PMID:3030813

A;Accession: A26646

A;Molecule type: mRNA

A;Residues: 1-471,'U',473-810 <FOR>

A;Cross-references: UNIPARC:UPI00000D8B8; GB:X05199; NID:935530; PIDN:CAA28831_1; PID:

A;Experimental source: liver

R;Malinowski, D.P.; Sadler, J.B.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and

A;Reference number: 145961; MUND:9523311; PMID:6148961

plasmin (EC 3.4.21-7) precursor [validated] - human
N;Contains: angiostatin; microplasmin; plasminogen

C;Species: Homo sapiens (man)

C;Accession: A5229; I52242; R26649; I62738; 184690; S93735; A00929; A04627; A04625; A0,

R;Petersen, T.F.; Martzen, M.R.; Ichinose, A.; Davie, E.W.

J. Biol. Chem. 265, 6104-6111, 1990

A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibr

A;Reference number: A35229; MUND:90202879; PMID:2318848

A;Accession: A35229

A;Molecule type: DNA

A;Residues: 1-810 <PTP>

A;Cross-references: UNIPROT:PO0747; UNIPROT:Q9UBQ9; UNIPROT:Q9UM12; UNIPARC:UPI000016AB

A;Experimental source: Leukocyte; lung fibroblast

R;Margaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Ti

Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990

A;Title: Definition of the transcription initiation site of human plasminogen gene in 1,

A;Reference number: 152242; MUND:91097523; PMID:2268308

A;Accession: 152242

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-16 <MAIL>

A;Cross-references: UNIPARC:UPI0000062A8; GB:M62890; NID:9190092; PIDN:AAA36454_1; PID

F;Forssgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.

FEBS Lett. 213, 254-260, 1987

A;Title: Molecular cloning and characterization of a full-length cDNA clone for human p

A;Reference number: A26646; MUND:87162490; PMID:3030813

A;Accession: A26646

A;Molecule type: mRNA

A;Residues: 1-471,'U',473-810 <FOR>

A;Cross-references: UNIPARC:UPI00000D8B8; GB:X05199; NID:935530; PIDN:CAA28831_1; PID:

A;Experimental source: liver

R;Malinowski, D.P.; Sadler, J.B.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and

A;Reference number: 145961; MUND:9523311; PMID:6148961

A;Accession: 145961

A;Molecule type: DNA

A;Residues: 1-810 <PTP>

A;Cross-references: UNIPROT:PO0747; UNIPROT:Q9UBQ9; UNIPROT:Q9UM12; UNIPARC:UPI000016AB

A;Experimental source: liver

R;Malinowski, D.P.; Sadler, J.B.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and

A;Reference number: 145961; MUND:9523311; PMID:6148961

A;Accession: 145961

A;Molecule type: DNA

A;Residues: 1-810 <PTP>

- A;Reference number: S03735; MUID:81212097; PMID:7238497
 A;Accession: S03735
 A;Molecule type: protein
 A;Residue: 20-71; 'E',73-76

 A;Cross-references: UNIPARC:UPI000017288C
 R;Sottrup-Jensen, L.; Petersen, T.B.; Magnusson, S.
 submitted to the Atlas, July 1977
 A;Reference number: A00929
 A;Accession: A00929
 A;Molecule type: protein
 A;Residue: 20-71; 'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
 R;Wiman, B.
 Bur. J. Biochem. 76, 129-137, 1977
 A;Title: Primary structure of the B-chain of human plasmin.
 A;Reference number: A04627; MUID:77225245; PMID:142009
 A;Accession: A04627
 A;Molecule type: protein
 A;Residue: 58-810 <WI1>
 A;Cross-references: UNIPARC:UPI0000145039
 R;Wiman, B.; Wallen, P.
 Bur. J. Biochem. 50, 489-494, 1975
 A;Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla
 A;Reference number: A04625; MUID:75093329; PMID:122932
 A;Accession: A04625
 A;Molecule type: protein
 A;Residues: 20-50,'Q',51-71,'E',73-85,87-100 <WI2>
 A;Cross-references: UNIPARC:UPI000017288F
 R;Wiman, B.; Wallen, P.
 Eur. J. Biochem. 58, 539-547, 1975
 A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen the
 A;Reference number: A04626; MUID:76043692; PMID:126863
 A;Accession: A04626
 A;Molecule type: protein
 A;Residue: 483-507,'E',509-604 <WI3>
 A;Cross-references: UNIPARC:UPI000017288F
 R;Robbins, K.C.; Bernabe, F.; Arzadon, L.; Summaria, L.
 J. Biol. Chem. 248, 1631-1633, 1973
 A;Title: The primary structure of human plasminogen. II. The histidine loop of human pla
 A;Reference number: A92128; MUID:73149248; PMID:4694729
 A;Contents: annotation; active site
 R;Groskopf, W.R.; Summaria, L.; Robbins, K.C.
 J. Biol. Chem. 244, 3590-3597, 1969
 A;Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
 A;Reference number: A92048; MUID:69234739; PMID:4240117
 A;Contents: annotation; active site
 R;Troxler, M.; Vali, Z.; Patthy, L.
 J. Biol. Chem. 257, 7401-7406, 1982
 A;Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
 A;Reference number: A92382; MUID:82213905; PMID:6919539
 A;Contents: annotation; omega-aminocarboxylic acid binding sites
 R;Valli, Z.; Patthy, L.
 J. Biol. Chem. 259, 13690-13694, 1984
 A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
 A;Reference number: A92458; MUID:85054794; PMID:6094526
 A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
 R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehnzel, S.; McCance, S.G.;
 J. Biol. Chem. 271, 29461-29467, 1996
 A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferativ
 A;Reference number: A58811; MUID:97067211; PMID:8910613
 A;Contents: annotation
 R;Linen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
 Biochemistry 37, 4699-4702, 1998
 A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1 (M
 A;Reference number: A58812; MUID:9546733; PMID:9548733
 A;Contents: annotation
 R;Tuilinsky, A.; Mulcahy, A.M.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A;Reference number: A51341; PDB:1PK4
 A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
 submitted to the Brookhaven Protein Data Bank, July 1991
-
- A;Reference number: A51488; PDB:1PK4
 A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
 R;Mu, T.P.; Tulinsky, A.
 submitted to the Brookhaven Protein Data Bank, August 1993
 A;Reference number: A51011; PDB:1PKR
 A;Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
 R;Padmanabhan, K.; Tulinsky, A.
 submitted to the Brookhaven Protein Data Bank, April 1994
 A;Reference number: A52408; PDB:1PMK
 A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
 R;Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A;Reference number: A65244; PDB:1CREA
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R;Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A;Reference number: A65245; PDB:1CBB
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
 Biochemistry 30, 10576-10588, 1991
 A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 A
 A;Reference number: A58819; MUID:92031502; PMID:1657148
 A;Contents: annotation
 R;Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
 Biochemistry 30, 10589-10594, 1991
 A;Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
 A;Reference number: A3983; MUID:9211803; PMID:1310033
 A;Contents: annotation
 R;de Vos, A.M.; Ulrich, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.
 Biochemistry 31, 270-279, 1992
 A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.0
 A;Reference number: A65803; MUID:92031503; PMID:1657149
 A;Contents: annotation
 R;Stec, B.; Teeter, M.M.; Whilton, M.; Yamano, A.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A;Reference number: A65808; PDB:1KRN
 A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
 R;Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A;Reference number: A65804; PDB:1HPK
 A;Contents: annotation; conformation by (1)H-NMR
 R;Rejante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 927-937, 1994
 A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
 A;Reference number: S43655; MUID:94237157; PMID:8181475
 A;Contents: annotation; conformation by (1)H-NMR
 R;Rejante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 930-949, 1994
 A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminog
 A;Reference number: A58817; MUID:94237158; PMID:8181476
 A;Contents: annotation; conformation by (1)H-NMR
 C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many ot
 C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKIU a
 C;PIR:FGHGB).
 C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHU2) immediately af
 ter cleavage by alpha-2-antiplasmin. This results in the formation of two chains connected by
 two disulfide bonds. Without the inhibitor, the two chains are inactive.
 C;Comment: Microplasmin is formed by autoclytic cleavage of plasmin under artificial cond
 C;Comment: Stromeleyin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. Tc
 C;Genetics: GDB:PLG
 A;Cross-references: GDB:119499; OMM:173350
 A;Map position: 6q26.6q27
 A;Introns: 17/1, 62/2; 98/1; 136/2; 183/1; 223/2; 317/2; 366/1; 419/2; 480/1; 529
 C;Function:
 A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 R;Tuilinsky, A.; Wu, T.P.
 submitted to the Brookhaven Protein Data Bank, July 1991

F-1-96-/Domain: plasminogen-related protein precursor homology <PLPH>	Db	158 DGPQPCWCYTIDPPERFEDCIDIPECDECEDCHCUGENYDGKISKITMSGJUBCOAMDSQSPHAR
F-20-810-/Product: plasminogen #status experimental <PRO>	Qy	121 GYPSKPKPNKLKKNYCNPDRELRPWCPTDPRCTPPSSGPTYQCLK
F-20-96-/Domain: activation peptide #status experimental <APT>	Db	218 GYPSKPKPNKLKKNYCNPDGSPRCPCTDPNKRMLCDTPRCTTPSSGPTYQCLK
F-79-466-/Product: angiotensin II receptor experimental <AST>	Qy	181 GTGENYGRVAVTVSGHCOHNSAQTPHTERUPENFCKNDENYCRNPDKGRAPWMT
F-97-580-/Product: plasmin #status experimental <MAT>	Db	240 GTGENYGRGDAVTVSGHCOHNSAQTPHTNRTPENFCKNDENYCRNPDKSEKAPWCYT
F-103-181-/Domain: kringle homology <KR1>	Qy	337 GTGENYGRVAVTVSGHCOHNSAQTPHTNRTPENFCKNDENYCRNPDKSEKAPWCYT
Query Match 99.7%; Score 1535; DB 1; Length 810; Best Local Similarity 99.6%; Pred. No. 1-68-104; Mismatches 0; Indels 0; Gaps 0;	Db	241 TNSQVRWBYCKPKSCDSPV
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy	338 TNSQVRWBYCKPKSCDSPV 357
RESULT 2		
B30848		
Plasmin (EC 3.4.21.7) precursor - rhesus macaque		
C:Species Macaca mulatta (rhesus macaque)		
C:Keywords fibrinolytic, plasminogen, protease, serine protease		
C:Accession: B32069; B30848		
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.		
J. Biol. Chem. 264, 5357-5365, 1989		
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.		
A:Reference number: A32869; MUID:89174660; PMID:2925643		
A:Accession: B32069		
A:Status: preliminary		
A:Molecule type: mRNA		
A:Residues: 1-810 <TOM>		
A:Cross-references: UNIPROT:P12545; UNIPARC:UPI0000131C0P; GB:J04697; NID:9342272; P10N: C:Superfamily: plasmin; kringle homology; Plasminogen-related protein precursor homology		
C:Keywords: fibrinolysis; glycoprotein; hydrolysis; kringle; serine proteinase		
F-1-96-/Domain: plasminogen-related protein precursor homology <PLPH>		
F-1-9-/Domain: signal sequence #status predicted <SIG>		
F-103-181-/Domain: kringle homology <KR1>		
F-185-262-/Domain: kringle homology <KR2>		
F-275-352-/Domain: kringle homology <KR3>		
F-377-454-/Domain: kringle homology <KR4>		
F-481-560-/Domain: kringle homology <KR5>		
F-581-803-/Domain: trypsin homology <TRY>		
F-581-73, 53-61, 103-181, 124-164, 152-176, 188-262, 188-316, 206-245, 234-257, 275-352, 296-335, 322 bonds: #status predicted		
F-622, 665, 760/Active site: His, ASP, Ser #status predicted		
Query Match 93.6%; Score 1442; DB 2; Length 810; Best Local Similarity 93.1%; Pred. No. 9-48-98; Mismatches 9; Indels 0; Gaps 0;		
Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;		
1 VVLSKECKTONGKNYRGTMKSKTKQITCQWSSTSPPHRSPATHPSGLEENYCRNPDN 60		
98 VVLSKECKTONGKNYRGTMKSKTKQITCQWSSTSPPHRSPATHPSGLEENYCRNPDN 157		
61 DPGQPWCYTIDPBRKRYDCDILECEECMHCSGYNDGKISKTMGJECQAWDSQSPHAR 120		
RESULT 3		
B30848		
Plasmin (EC 3.4.21.7) precursor - pig (fragment)		
N:Alternate names: plasminogen		
N:Contain: miniplasminogen		
C:Species: Sus scrofa domesticus (domestic pig)		
C:Accession: S03733; S03737; K5834		
R;Schaller, J.; Marti, T.; Roesellet, S.J.; Kampfer, U.; Rickli, E.		
Fibrinolysis 1, 91-102, 1987		
A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the c		
Eur. J. Biochem. 114, 465-470, 1981		
A:Reference number: S03733		
A:Accession: S03733		
A:Molecule type: Protein		
A:Residues: 1-560 <SCH>		
A:Cross-references: UNIPROT:P08867; UNIPARC:UPI0000172B90		
R;Bruunsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.B.; Lergier, W.; Manneberg, M.,		
Eur. J. Biochem. 114, 465-470, 1981		
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,		
A:Reference number: S03735; MUID:81212097; PMID:7238497		
A:Accession: S03737		
A:Molecule type: protein		
A:Residues: 1-57 <BRU>		
A:Cross-references: UNIPARC:UPI0000172B91		
R;Marti, T.; Schaller, J.; Rickli, E.B.		
Eur. J. Biochem. 149, 27-285, 1985		
A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.		
A:Reference number: A25834; MUID:85203907; PMID:3846533		
A:Accession: A25834		
A:Molecule type: protein		
A:Residues: 450-790 <MAR>		
A:Cross-references: UNIPARC:UPI0000172B92		
C:Function:		
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator		
A:Pathway: fibrinolysis		
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology		
C:Keywords: fibrinolysis; glycoprotein; hydrolysis; kringle; kidney; plasma; serine protease		
F-1-77-/Product: plasminogen #status predicted <PRO>		
F-1-77-/Domain: activation peptide #status predicted <APT>		
F-78-550-/Product: plasmin chain A #status predicted <ACT>		
F-84-162-/Domain: kringle homology <KR1>		
F-166-243-/Domain: kringle homology <KR2>		
F-256-333-/Domain: kringle homology <KR3>		
F-358-435-/Domain: kringle homology <KR4>		
F-450-790-/Product: miniplasminogen #status experimental <MIN>		
F-461-540-/Domain: kringle homology <KR5>		
F-561-790-/Product: plasmin chain B #status experimental <BCH>		
F-561-783-/Domain: trypsin homology <TRY>		
F-530-54-34-42, 84-162, 105-45, 113-157, 166-243, 169-297, 187-226, 215-238, 256-333, 277-316, 305- bonds: #status predicted		
F-602-645-740/Active site: His, ASP, Ser #status predicted		
Query Match 83.9%; Score 1292; DB 1; Length 790; Best Local Similarity 81.4%; Pred. No. 88-87; Mismatches 23; Indels 0; Gaps 0;		
Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;		

eful in treating solid tumors.

C;Function:

A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator pathway: fibrinolysis

C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis; plasminogen-related protein precursor homology <PPH>

F;185-262;/domain: kringle homology <KR2>
F;275-352;/domain: kringle homology <KR3>
F;379-456;/domain: kringle homology <KR4>
F;482-561;/domain: kringle homology <KR5>

F;20-812;/Product: plasminogen #status predicted <SIG>
F;20-96;/Domain: activation peptide #status predicted <APM>
F;79-466;/Product: angiotensin II #status predicted <AST>

F;97-581,582-812;/Product: plasmin #status predicted <MAT>
F;1-19;/Domain: chain A #status predicted <ACH>
F;1-181;/Domain: chain B #status predicted <BCH>

F;185-262;/domain: kringle homology <KR2>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32 bonds: #status predicted

F;78-79;/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
F;136-308;/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;466-467;/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F;581-582;/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F;624,667,762;/Active site: His, Asp, Ser #status predicted

Query Match 82.7%; Score 1274; DB 1; Length 812;
Best Local Similarity 80.6%; Pred. No. 1.7e-05;
Matches 208; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

Qy 1 VVLSCECKTGNGKNGYRGMSTKNGITOKWKSSTSPPHRPRFSPATHSEGLENYCNPDN 60
Db 98 VVLSCECKTGNGKNGYRGMSTKNGITOKWKSSTSPPHRPRFSPATHSEGLENYCNPDN 157

Qy 61 DROGPWMWTTDPERKRYVCDLCECEBOMHSSEGENDGKSKTMSGLCQWADSDOPHAH 120
Db 158 DROGPWMWTTDPERKRYVCDLCECEBOMHSSEGENDGKSKTMSGLCQWADSDOPHAH 217

Qy 121 GYPSKEPKPNKLUKNKNCNCRNPDRBLPWCPTDPNKGWELCDIPRCCTTPPSSGPTVQLK 180
Db 218 GYPSKEPKPNKLUKNKNCNCRNPDRBLPWCPTDPNKGWELCDIPRCCTTPPSSGPTVQLK 277

Qy 181 GTCGENTYGNVAVTVSGTCQHSAQPTHTHERPTPENPKCNUDENCCRNPDKRAWCHT 240
Db 278 GNGEHTGNAVATVSGTCQHSAQPTHTHERPTPENPKCNUDENCCRNPDKRAWCHT 337

Qy 241 TNSQVRWBYCKIPSCDSS 259
Db 338 TNSSVRWBYCKIPSCDSS 355

RESULT 7

T18518 apolipoprotein(a) - western European hedgehog (fragment)
C;Species: *Erinaceus europaeus* (western European hedgehog)
C;Accession: T18518 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Lawn, R.M.; Boomkamp, N.W.; Schwartz, K.; Lindahl, G.B.; Wade, D.P.; Byrne, C.D.; Fong, J.; Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein(a); Reference number: 146259; PMID: 96025778; PMID: 7592597
A;Accession: T18518
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2869 <LW>
A;Cross-references: UNIPROT:Q28398; UNIPARC:UPI000008785C; EMBL:U33170; NID:91046358; PIR: P05300
A;Experimental source: Liver
C;Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, contains apolipoprotein(a).

Query Match 57.2%; Score 881; DB 2; Length 2869;
Best Local Similarity 55.0%; Pred. No. 2.7e-56;
Matches 149; Conservative 36; Mismatches 70; Indels 16; Gaps 3;

Qy 3 LSECKTGNGKNGYRGMSTKNGITOKWKSSTSPPHRPRFSPATHSEGLENYCNPDN 62
Db 2495 VDQCLGTTGEGNRGAVAVTAAGTCRWRCSPHSISRTPENYPTONLVGCRNGR- 2553

Qy 63 QWPWCYTDTPERKRYVCDLCEBOMHSSEGENDGKSKTMSGLCQ 110
Db 2554 VWPWCYTTSAMRWEECCSIPACESPPTPTEHLVVPQCLEGENDGKSKTMSGLCQ 2613

Qy 111 AWDSOSPHAKYIPTSKPNKLUKNKNCNCRNPDRBLPWCPTDPNKGWELCDIPRCCTTPP 170
Db 2614 GWRKQFHFRHETPENPKCNUDENCCRNPDKRAWCHT 2673

Qy 171 SSGPTV--OQKGTYGNGYRGMSTKNGITOKWKSSTSPPHRPRFSPATHSEGLENYC 227
Db 2674 PTPEPMIIPDOLCGTGHENYGRGAVAVTSGTCQHSAQPTHTHERPTPENPKCNUDENCCRNPDKRAWCHT 2733

Qy 228 RNPDGKRAPWCHTTNSQVRWBYCKIPSCDSS 258
Db 2734 RNPGEVWAPWCYTTSAMRWEECCSIPACESPPTPTEHLVVPQCLEGENDGKSKTMSGLCQ 2764

RESULT 6

146250 plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: *Erioloides europaeus* (western European hedgehog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I16260
R;Lawn, R.M.; Boomkamp, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J.; Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein(a); Reference number: 146259; PMID: 96025778; PMID: 7592597
A;Accession: I16260
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Residues: 1-2810 <LW>
A;Cross-references: UNIPROT:Q29485; UNIPARC:UPI00001310CD; EMBL:U33171; NID:91046360; PIR: P05300
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine protease
F;1-96;/Domain: plasminogen-related protein precursor homology <PPH>
F;103-181;/Domain: kringle homology <KR1>

RESULT 8

JH0579 hepatocyte growth factor precursor [validated] - human
 N;Alternative names: hepatocyte growth factor precursor [validated] - human
 C;Species: Homo sapiens (man)
 C;Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text change 09-Jul-2004
 C;Accession: JH0579; JU033; A4110; B36677; A33512; A29006; PH0114; A37796; SOS
 R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
 Gene 102, 213-219, 1991
 A;Title: Organization of the human hepatocyte growth factor-encoding gene.
 A;Reference number: JH0579; MUID:91340155; PMID:1831432
 A;Accession: JH0579
 A;Molecule type: DNA
 A;Residues: 1-728 <SEK>
 A;Cross-references: UNIPROT:PI4210; UNIPARC:UPI00000092B; DDBJ:D90318
 A;Note: the authors submitted the codon GAA for residue 662 as GIV
 R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
 A;Reference number: JU0333
 A;Accession: JU0333
 A;Molecule type: DNA
 A;Residues: 1-481; RT; '494-728 <SEK>
 A;Cross-references: UNIPARC:UPI00000092B
 R;Weddner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
 Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
 A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor
 A;Reference number: A4110; MUID:9133493; PMID:1831265
 A;Accession: A4110
 A;Molecule type: mRNA
 A;Residues: 1-728 <SEK>
 A;Cross-references: UNIPARC:UPI00000092B; GB:M73239; NID:9337935; PIDN:AAA64239.1; PID:
 R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
 Biochem. Biophys. Res. Commun. 172, 321-327, 1990
 A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor
 A;Reference number: A36677; MUID:91025062; PMID:2145836
 A;Molecule type: mRNA
 A;Residues: 1-28 <SE3>
 A;Cross-references: UNIPARC:UPI00000092B; GB:M60718; NID:9184031; PIDN:AAA52648.1; PID:
 A;Accession: A36677
 A;Molecule type: mRNA
 A;Residues: 1-61; 167-728 <SE4>
 A;Cross-references: UNIPARC:UPI0000146316; EMBL:X16323
 A;Experimental source: leukocyte
 R;Miyazawa, K.; Tsabouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya,
 Biochem. Biophys. Res. Commun. 163, 967-973, 1989
 A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor
 A;Reference number: A33512; MUID:89392017; PMID:2528952
 A;Accession: A33512
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1728 <MY>
 A;Cross-references: UNIPARC:UPI00000092B; GB:M29145; NID:9184041; PIDN:AAA52650.1; PID:
 R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
 proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
 A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte
 A;Reference number: A39006; MUID:91110540; PMID:1834873
 A;Accession: A39006
 A;Molecule type: mRNA
 A;Residues: 1-161; 167-728 <RUB>
 A;Cross-references: UNIPARC:UPI0000146316; GB:M55379
 A;Experimental source: embryonic lung
 R;Yoshimura, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
 Biochem. Biophys. Res. Commun. 175, 660-667, 1991
 A;Title: Identification of the N-terminal residue of the heavy chain of both native and
 A;Reference number: PH0114; MUID:91207365; PMID:1826837
 A;Molecule type: protein
 A;Residues: 32-43; 53-58 <YOS>
 A;Cross-references: UNIPARC:UPI0000172B98; UNIPARC:UPI0000172B99

A;Experimental source: plasma
 R;Weidner, K.M.; Behrens, J.; Birchmeier, W.
 J. Cell Biol. 111, 2097-2108, 1990
 A;Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
 A;Reference number: A37796; MUID:91035621; PMID:2146276
 A;Accession: A37796
 A;Molecule type: protein
 A;Residues: 86-91; 329-344; 356-363; 'XX'; 366-370; 425-424; 442-447; 'X'; 449-450; 543-546; 'X'; 5
 A;Cross-references: UNIPARC:UPI0000172B9A; UNIPARC:UPI0000172BB; UNIPARC:UPI0000172BC
 R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashi
 Nature 342, 440-443, 1990
 A;Title: Molecular cloning and expression of human hepatocyte growth factor.
 A;Reference number: SOS
 A;Accession: SOS6794; MUID:90066676; PMID:2531289
 A;Accession: SOS6794
 A;Molecule type: mRNA
 A;Residues: 1-31; 'HK'; 34-77; 'N'; 79-292; 'V'; 294-299; 'W'; 301-316; 'A'; 318-335; 'K'; 337-386'
 A;Note: part of this sequence, including the amino acid of both the alpha and beta chains
 R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachse, M.; Vigna, E.; Comoglio, P.M.; Birch
 Proc. Natl. Acad. Sci. U.S.A. 89, 1154-1158, 1992
 A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
 A;Reference number: 15914; MUID:93087571; PMID:2280330
 A;Accession: 159214
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-288; 'ET'; <HAR>
 A;Cross-references: UNIPARC:UPI000073BF9; GB:L02931; NID:9184033; PIDN:AAA52649.1; PID:
 R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
 Eur. J. Biochem. 197, 15-22, 1991
 A;Title: An alternatively processed mRNA generated from human hepatocyte growth factor
 A;Reference number: S15443; MUID:91200041; PMID:1826653
 A;Accession: S15443
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-288; 'ET'; <MIY>
 A;Cross-references: UNIPARC:UPI000073BF9; EMBL:X57574; NID:932083; PIDN:CAA40802.1; PID:
 R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuwa, E.; Murakami, A.; Higashio, K.
 Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
 A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
 A;Reference number: 152253; MUID:22062058; PMID:1833983
 A;Accession: 152253
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 161-166 <SH>
 A;Cross-references: UNIPARC:UPI0000353AB; GB:S62561; NID:9237996; PIDN:AAB20169.1; PID:
 C;Genetics:
 A;Gene: GDB:HGP
 A;Cross-references: GDB:127524; OMIM:142409
 A;Map position: 7q21.1-q21.1
 A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 48
 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C;Function:
 A;Description: stimulates mitosis of hepatocytes and other cells
 A;Note: does not have protease activity
 C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
 C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;32-494; 495-728/Domain: hepatocyte growth factor #status experimental <MAT>
 F;32-494/Domain: alpha chain #status experimental <ACH>
 F;128-226/Domain: kringle homology <KR1>
 F;211-288/Domain: kringle homology <KR2>
 F;305-383/Domain: kringle homology <KR3>
 F;311-469/Domain: kringle homology <KR4>
 F;495-728/Domain: beta chain #status experimental <BCH>
 F;495-728/Domain: trypsin homology <TRY>
 F;32/Modified site: Pyrrolidine carboxylic acid (Gln) (in mature form) #status experimen
 F;294-402; 556-653/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;487-604/Disulfide bonds: #status predicted

Query Match Best Local Similarity Score DB 1; Length 728;

QY	240	TINNSQVRHIC-KIPSCSS	258
N;Alternate names:	hepatopoitin	A; scatter factor	
C;Species:	Mus musculus (house mouse)		
C;Date:	03-Mar-1993	#sequence revision	26-May-1994 #text change 09-Jul-2004
C;Accession:	JC2117; PC2064; A60185; S43416; S15521; S17173; S10966; I40758; JU0231		
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Bianni, J.			
Biochem. Biophys. Res. Commun. 199, 772-779, 1994			
A;Title:	Identification of mouse mammary fibroblast-derived mammary growth factor as hepatocyte growth factor/scatter factor		
A;Reference number:	JC2117; MUID:94183257; PMID:18135822		
A;Accession:	JC2117		
A;Molecule type:	mRNA		
A;Residues:	1-728 <SAS2>		
A;Cross-references:	UNIPARC:UPI0000172BA1		
A;Experimental source:	fibroblast; COS-1 cell		
A;Note:	submitted to JIPID, May 1993		
A;Molecule type:	protein		
A;Residues:	496-504 <SA2>		
A;Cross-references:	UNIPARC:UPI0000172BA1		
R;Rosen, E.M.; Marcovsky, L.; Setter, E.; Winter, D.W.; Goldberg, I.D.			
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990			
A;Title:	Purified scatter factor stimulates epithelial and vascular endothelial cell migration		
A;Reference number:	A60185; MUID:90377927; PMID:2144630		
A;Accession:	A60185		
A;Molecule type:	protein		
A;Residues:	'X', 184-188, 'KX', 191-192, 'X', 194, 'XX', 197-357-364, 'XX', 367-375-377, 'R', 379,		
A;Cross-references:	UNIPARC:UPI0000172BA2; UNIPARC:UPI0000172BA3; UNIPARC:UPI0000172BA4;		
R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.			
Biochim. Biophys. Acta 1216, 299-303, 1993			
A;Title:	Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth factor/scatter factor		
A;Reference number:	S43416; MUID:94060105; PMID:8241272		
A;Accession:	S43416		
A;Status:	preliminary		
A;Molecule type:	mRNA		
A;Residues:	1-728 <LIU>		
A;Cross-references:	UNIPARC:UPI000000084; EMBL:X72307		
R;Liu, Y.			
submitted to the EMBL Data Library, May 1993			
A;Reference number:	S45521		
A;Status:	preliminary		
A;Molecule type:	mRNA		
A;Residues:	1-563, 'H', 565-728 <LIU>		
A;Cross-references:	UNIPARC:UPI0000172BA6; EMBL:X72307		
R;Cotter, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.			
Biochem. J. 278, 35-41, 1991			
A;Title:	Purification and characterization of biologically active scatter factor from rat liver		
A;Reference number:	S17173; MUID:91354223; PMID:1831975		
A;Accession:	S17173		
A;Molecule type:	protein		
A;Residues:	496-517, 'T', 519 <COF>		
A;Cross-references:	UNIPARC:UPI0000172BA7		
R;Gherardi, E.; Stoker, M.			
Nature 346, 228, 1990			
A;Title:	Hepatocytes and scatter factor		
A;Reference number:	S10966; MUID:90326152; PMID:2142751		
A;Accession:	S10966		
A;Status:	preliminary		
A;Molecule type:	protein		
A;Residues:	496-507, 'X', 509-512, 'L', 514-516, 'X', 518-519 <NAT>		
A;Cross-references:	UNIPARC:UPI0000172BA8		
R;Plaschke-Schlüter, A.; Beutens, J.; Gherardi, E.; Birchmeier, W.			
J. Biol. Chem. 270, 830-836, 1995			
A;Title:	Characterization of the scatter factor/hepatocyte growth factor gene promoter.		
A;Reference number:	I48758; MUID:95122532; PMID:782318		

A;Accession: I48758
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-30 <RES>
A;CROSS-references: UPID:UPI0000006DC; EMBL:X81630; NID:9673451; PIDN:CAAS57286.1; PI
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
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F-56-495,-496-728/Product: hepatocyte growth factor #status predicted <MAT>
F;6-495-/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207-/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-394/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;-96-728-/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: tryptin homology <TRY>
F;33-/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted
F;285,433,560,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted

F;489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCI>	RESULT 14
Best Local Similarity 49.8%; Score 766.5; DB 1; Length 716; Pred. No. 1.5e-48; Mismatches 89; Indels 15; Gaps 5; Matches 132; Conservative 36; Mismatches 89; Indels 15; Gaps 5; Mismatches 132; Conservative 36; Mismatches 89; Indels 15; Gaps 5; Matches 132; Conservative 36; Mismatches 89; Indels 15; Gaps 5;	A40332
Query Match 2 YLSECKTGKNGKRYGRTMSKTRGKTCOKWSSTSPPHRPRSPATHPSBEGLEENYCRNPND 61	N;Alternate names: hepatocyte growth factor-like protein
Db 106 YVRTCIMDNGASYRGTVARTADGILPCQAWSRRPFDHKYPT--PKNGLBNFCRNPDG 163	C;Species: Mus musculus (house mouse)
Qy 62 PQQPWCYTIDPEKRYDYCDILECEE-CMHCSCENYDKISKMSGLEQAMQSOSPAH 120	C;Accession: A40332; B40332
Db 164 PRGPWCYTNSVRFQSGIKSCREAVCUCWMCINGEDYRGDVDTESGRECBORMDLQPHSH 223	R;Degen, S.J.R.; Stuart, L.A.; Han, S.; Jamison, C.S.
Qy 121 GYISKEPKPNKJNKYCNPDRBLRPPWCFTDENKRWECDIIPRC--TTPPSSGGPYQ- 177	Biochemistry 30, 9781-9791, 1991
Db 224 PRHPBKEDPKAKJNDYCNPDASERPWXYTDPNVEREFCDLRSQGPNLPLPTVGSKSQ 283	A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor
Qy 178 -----CLKGATGENTRGNVAVTWSGHTQHWAQTPTHTERTPENPPCKNDENYCRN 229	A;Reference number: A40332; MUID:92002017; PMID:1832957
Db 284 RNKVKAQNCFRGKEDYRGTTNTSAGVPCQRMQDAONPHORFVPEKYACKDOLRENFCRN 343	A;Accession: A40332
Qy 230 PDGKRAPWCHTNQVWRWCYK-KIPSCDSSPV 260	A;Residues: 1-18, 'P', 20-716 <DEG2>
Db 344 PDGSEAPWCFTSRGLRVAFCVQIPRCTEEVV 375	A;Molecule type: DNA
RESULT 13	A;Cross-references: UNIPARC:UPI00000402E; GB:M74180; NID:9193831; PID:
151285 hepatocyte growth factor/scatter factor - chicken (fragment)	C;Genetics: A;Cross-references: UNIPROT:P26928; UNIPARC:UPI00000402E; GB:M74180; NID:9193831; PID:
C;Species: Gallus gallus (chicken)	A;Accession: B40332
C;Date: 13-Sep-1995 #Sequence_revision 13-Sep-1996 #text_change 09-Jul-2004	A;Molecule type: mRNA
C;Accession: 151285	A;Residues: 1-18, 'P', 20-716 <DEG>
R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherardini, C.;Development: 121, 812-824, 1995	A;Cross-references: UNIPARC:UPI000027E40; GB:M74181; NID:9193833; PID:
A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node during development	C;Accession: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 471/2; 510/2; 548/1; 587/2; 626/1; 664/2; 703/2; 741/2; 779/2; 817/2; 855/2; 893/2; 931/2; 969/2; 1007/2; 1045/2; 1083/2; 1121/2; 1159/2; 1197/2; 1235/2; 1273/2; 1311/2; 1349/2; 1387/2; 1425/2; 1463/2; 1501/2; 1539/2; 1577/2; 1615/2; 1653/2; 1691/2; 1729/2; 1767/2; 1805/2; 1843/2; 1881/2; 1919/2; 1957/2; 1995/2; 2033/2; 2071/2; 2109/2; 2147/2; 2185/2; 2223/2; 2261/2; 2309/2; 2347/2; 2385/2; 2423/2; 2461/2; 2509/2; 2547/2; 2585/2; 2623/2; 2661/2; 2709/2; 2747/2; 2785/2; 2823/2; 2861/2; 2909/2; 2947/2; 2985/2; 3023/2; 3061/2; 3109/2; 3147/2; 3185/2; 3223/2; 3261/2; 3309/2; 3347/2; 3385/2; 3423/2; 3461/2; 3509/2; 3547/2; 3585/2; 3623/2; 3661/2; 3709/2; 3747/2; 3785/2; 3823/2; 3861/2; 3909/2; 3947/2; 3985/2; 4023/2; 4061/2; 4109/2; 4147/2; 4185/2; 4223/2; 4261/2; 4309/2; 4347/2; 4385/2; 4423/2; 4461/2; 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A;Cross-references: UNIPROT:PO8519; UNIPARC:UPI00001C499; GB:X06290; EMBL:X0696; NID:9
R;Eaton, D.L.; Pless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A;Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A;Reference number: A28017; MUID:87204109; PMID:3472206
A;Accession: A28017
A;Molecule type: protein
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X', 4396-4701 <EMT>
A;Cross-references: UNIPARC:UPI0000172BB0; UNIPARC:UPI0000172BB1; UNIPARC:UPI0000172BB2;
R;Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A;Title: 5' control regions of the apolipoprotein(a) gene and members of the related pla
A;Reference number: A47277; MUID:9316568; PMID:7679504
A;Accession: A47277
A;Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Note: apo(a) gene 1 (nomenclature of reference 152415)
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A;Cross-references: UNIPARC:UPI0000062AB; GB:M90079; NID:9178784; PIDN:AAA35546.1; PID:
R;Ichinose, A., 3113-3118, 1992
Biochemistry 31, 3113-3118, 1992
A;Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wi
A;Reference number: I52415; MUID:92207924; PMID:154698
A;Accession: I52415
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-16 <RE3>
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A;Note: apo(a) gene 1 (nomenclature of reference 152415)
A;Accession: I52286
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPARC:UPI0000062AB; GB:M86878; NID:9178782; PIDN:AAA51749.1; PID:
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A;Cross-references: GDB:120699; OMIM:152200
A;Map position: 6q26.6q27
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C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
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F484-561/Domain: kringle homology <KR5>
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F1-4328-4541/Domain: trypsin homology <TRY>

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Db 4018 YRGISSTIVTRCTCOSWSSMIPHWKORTPENIPNAGLITENCRNFDGKQPWCYTDPV 4077
QY 246 RWEYKPKPSQCS 258
Db 4078 RWEYCNLTCSET 4090

Search completed: January 25, 2006, 17:10:57
Job time : 40 secs

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: January 25, 2006, 17:11:02 ; Search time 32 Seconds

87.986 Million cell updates/sec

Title: US-09-502-176-2

Perfect Score: 1540

Sequence: 1 VYLSECKTGNGKNGYRGTMSK..... TNSQVRMVBCKLIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1535	99.7	339	7 US-11-010-874-3
2	1535	99.7	567	6 US-10-995-561-764
3	1535	99.7	791	7 US-11-056-621-4
4	1535	99.7	810	6 US-10-995-561-761
5	1535	99.7	810	6 US-11-020-824-2
6	1442	93.6	339	7 US-11-010-874-4
7	1296	84.2	339	7 US-11-010-874-6
8	1292	83.9	339	7 US-11-010-874-5
9	1274	82.7	339	7 US-11-010-874-2
10	1274	82.7	812	7 US-11-010-874-1
11	1001	65.0	168	7 US-11-010-874-8
12	954	61.9	168	7 US-11-010-874-9
13	952	61.8	160	7 US-11-010-874-13
14	896	58.2	160	7 US-11-010-874-14
15	883	57.3	168	7 US-11-010-874-10
16	881	57.2	168	7 US-11-010-874-11
17	847	55.0	168	7 US-11-010-874-8
18	801	52.0	160	7 US-11-010-874-16
19	799	51.9	160	7 US-11-010-874-15
20	797	51.8	160	7 US-11-010-874-12
21	797	51.8	728	7 US-11-024-635-6
22	797	51.8	728	7 US-11-124-635-8
23	797	51.8	728	7 US-11-043-788-164
24	749	48.6	1169	6 US-10-995-561-609
25	749	48.6	1169	7 US-11-124-368A-228

ALIGNMENTS

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RESULT 1
US-11-010-874-3
; Sequence 3, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: S820-656
; CURRENT APPLICATION NUMBER: US/11/010-874
; CURRENT FILING DATE: 2004-12-13
; PRIORITY APPLICATION NUMBER: 10/963,115
; PRIORITY FILING DATE: 2004-10-12
; PRIORITY APPLICATION NUMBER: 60/510,620
; PRIORITY FILING DATE: 2003-10-10
; PRIORITY APPLICATION NUMBER: 60/528,647
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-010-874-3
Query Match 99.7%; Score 1535; DB 7; Length 339;
Best Local Similarity 99.6%; Pred. No. 6.2e-119; Mismatches 0; Gaps 0; Indels 0;
Matches 259; Conservative 0; Sensitive 0; Sequence 3, Appli
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Sequence 286, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 287, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 288, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 289, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 290, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 291, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 292, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 293, 61 DPOGPWVTTDEPKRYCQKSKTMSGLCQAWDSOPRAH
Sequence 294, 61 D
```

RESULT 2

US-00-995-561-764

; Sequence 764, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995, 561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 764

; LENGTH: 567

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-00-995-561-764

Query Match 99.7%; Score 1535; DB 6; Length 567;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBCKTGKNGNYRGTMSKTKGKTSKTMGSSTSPHRPRSPATHPSSEGLENCRNPDN 60

Db 79 VYLSBCKTGKNGNYRGTMSKTKGKTSKTMGSSTSPHRPRSPATHPSSEGLENCRNPDN 138

Qy 61 DPGQWMTTDEPEKYDQILECERCMCMSGENDGKISKTMGSLECAWDSDSPHAN 120

Db 139 DPGQWMTTDEPEKYDQILECERCMCMSGENDGKISKTMGSLECAWDSDSPHAN 198

Qy 121 GYIPSKFPNKNLKKYCRNPFDRLLPWCFTDPNKRWECLIPRCTTPPSGGPTYQCLK 180

Db 199 GYIPSKFPNKNLKKYCRNPFDRLLPWCFTDPNKRWECLIPRCTTPPSGGPTYQCLK 258

Qy 181 GTGENYRGNVAVTWSGHTCWSACTPHTERTPENPKNLDENYCRNPDGRAPWCHT 240

Db 259 GTGENYRGNVAVTWSGHTCWSACTPHTERTPENPKNLDENYCRNPDGRAPWCHT 318

Qy 241 TNSQVRWEYCKIPSCDSSPV 260

Db 319 TNSQVRWEYCKIPSCDSSPV 338

; US-11-056-621-4

Query Match 99.7%; Score 1535; DB 7; Length 791;

Best Local Similarity 99.6%; Pred. No. 1.4e-118; Length 791;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBCKTGKNGNYRGTMSKTKGKTSKTMGSSTSPHRPRSPATHPSSEGLENCRNPDN 60

Db 79 VYLSBCKTGKNGNYRGTMSKTKGKTSKTMGSSTSPHRPRSPATHPSSEGLENCRNPDN 138

Qy 61 DPGQWMTTDEPEKYDQILECERCMCMSGENDGKISKTMGSLECAWDSDSPHAN 120

Db 139 DPGQWMTTDEPEKYDQILECERCMCMSGENDGKISKTMGSLECAWDSDSPHAN 198

Qy 121 GYIPSKFPNKNLKKYCRNPFDRLLPWCFTDPNKRWECLIPRCTTPPSGGPTYQCLK 180

Db 199 GYIPSKFPNKNLKKYCRNPFDRLLPWCFTDPNKRWECLIPRCTTPPSGGPTYQCLK 258

Qy 181 GTGENYRGNVAVTWSGHTCWSACTPHTERTPENPKNLDENYCRNPDGRAPWCHT 240

Db 259 GTGENYRGNVAVTWSGHTCWSACTPHTERTPENPKNLDENYCRNPDGRAPWCHT 318

Qy 241 TNSQVRWEYCKIPSCDSSPV 260

Db 338 TNSQVRWEYCKIPSCDSSPV 357

US-11-056-621-4

Query Match 99.7%; Score 1535; DB 7; Length 791;

Best Local Similarity 99.6%; Pred. No. 1.4e-118; Length 791;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBCKTGKNGNYRGTMSKTKGKTSKTMGSSTSPHRPRSPATHPSSEGLENCRNPDN 60

Db 79 VYLSBCKTGKNGNYRGTMSKTKGKTSKTMGSSTSPHRPRSPATHPSSEGLENCRNPDN 138

Qy 61 DPGQWMTTDEPEKYDQILECERCMCMSGENDGKISKTMGSLECAWDSDSPHAN 120

Db 139 DPGQWMTTDEPEKYDQILECERCMCMSGENDGKISKTMGSLECAWDSDSPHAN 198

Qy 121 GYIPSKFPNKNLKKYCRNPFDRLLPWCFTDPNKRWECLIPRCTTPPSGGPTYQCLK 180

Db 199 GYIPSKFPNKNLKKYCRNPFDRLLPWCFTDPNKRWECLIPRCTTPPSGGPTYQCLK 258

Qy 181 GTGENYRGNVAVTWSGHTCWSACTPHTERTPENPKNLDENYCRNPDGRAPWCHT 240

Db 259 GTGENYRGNVAVTWSGHTCWSACTPHTERTPENPKNLDENYCRNPDGRAPWCHT 318

Qy 241 TNSQVRWEYCKIPSCDSSPV 260

Db 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 3

US-11-056-621-4

; Sequence 4, Application US/11056621

; GENERAL INFORMATION:

; APPLICANT: Spincer, David

; APPLICANT: Spencer, Lynn F.

; APPLICANT: Gasdaska, John R.

; APPLICANT: Wang, Xiaowei

; APPLICANT: Cox, Kevin M.

; APPLICANT: Peels, Charles G.

; TITLE OF INVENTION: EXPRESSION OF PLASMINOGEN AND

; TITLE OF INVENTION: MICROPLASMINOGEN IN DUCKWEED

; FILE REFERENCE: 40989/274646

; CURRENT APPLICATION NUMBER: US/11/056, 621

; CURRENT FILING DATE: 2005-02-11

; PRIOR APPLICATION NUMBER: US 60/543, 487

; PRIOR FILING DATE: 2004-02-11

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 791

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Sequence of mature human plasminogen

; FEATURE:

; RESULT 5

US-10-220-824-2
; Sequence 2, Application US/10220824
; Publication No. US20050277603A1
; GENERAL INFORMATION:
; APPLICANT: VIROMED Limited
; TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including a gene encoding an anti-angiogenic protein or parts thereof
; FILE REFERENCE: OPF0208/PCT
; CURRENT APPLICATION NUMBER: US/10/220,824
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: KR 2001-0000691
; PRIORITY FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 2 :
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-220-824-2

Query Match 99.7%; Score 1535; DB 6; Length 810;
Best Local Similarity 99.6%; Pred. No. 1.4e-18; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMKTKNGTICQKWSSTSPPRSPATHSEGLENYCNPDN 60
Db 1 VYLSECKTGNGKNYRGTMKTKNGTICQKWSSTSPPRSPATHSEGLENYCNPDN 60

QY 61 DPOGPKCYTTPPEKRVDYCDLCECERCMHSGENTDGKSKTMSGLCQAWDSOPRAH 120
Db 61 DPOGPKCYTTPPEKRVDYCDLCECERCMHSGENTDGKSKTMSGLCQAWDSOPRAH 120

QY 121 GYPSKEPNKLUKNYCRNPDRLPWCFTTDPKWELCDIPRCTTPPSGGPTVCLK 180
Db 121 GYPSKEPNKLUKNYCRNPDRLPWCFTTDPKWELCDIPRCTTPPSGGPTVCLK 180

QY 181 GTGENTRGNVAVTVSGHTCQHSAQTPHTERTPENPCPKDLENCRNPDGRAPWCHT 240
Db 181 GTGENTRGNVAVTVSGHTCQHSAQTPHTERTPENPCPKDLENCRNPDGRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCSSPV 260
Db 241 TNSQVRWEYCKIPSCSSPV 260

RESULT 6
US-11-010-874-4
; Sequence 4, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820-656
; CURRENT APPLICATION NUMBER: US/11/010, 874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963, 115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510, 620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528, 647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6
; LENGTH: 339
; TYPE: PRT
; ORGANISM: bovine
; US-11-010-874-6

Query Match 84.2%; Score 1296; DB 7; Length 339;
Best Local Similarity 81.2%; Pred. No. 2.2e-99; Matches 211; Conservative 22; Mismatches 27; Indels 0; Gaps 0; Matches 211; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMKTKNGTICQKWSSTSPPRSPATHSEGLENYCNPDN 60
Db 1 VYLSECKTGNGKNYRGTMKTKNGTICQKWSSTSPPRSPATHSEGLENYCNPDN 60

QY 61 DPOGPKCYTTPPEKRVDYCDLCECERCMHSGENTDGKSKTMSGLCQAWDSOPRAH 120
Db 61 DPOGPKCYTTPPEKRVDYCDLCECERCMHSGENTDGKSKTMSGLCQAWDSOPRAH 120

QY 121 GYPSKEPNKLUKNYCRNPDRLPWCFTTDPKWELCDIPRCTTPPSGGPTVCLK 180
Db 121 GYPSKEPNKLUKNYCRNPDRLPWCFTTDPKWELCDIPRCTTPPSGGPTVCLK 180

QY 181 GTGENTRGNVAVTVSGHTCQHSAQTPHTERTPENPCPKDLENCRNPDGRAPWCHT 240
Db 181 GTGENTRGNVAVTVSGHTCQHSAQTPHTERTPENPCPKDLENCRNPDGRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCSSPV 260
Db 241 TNSQVRWEYCKIPSCSSPV 260

QY 241 TNSEVRWEYCTIPSCSSPL 260

RESULT 8
US-11-010-874-4
; Sequence 4, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820-656
; CURRENT APPLICATION NUMBER: US/11/010, 874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963, 115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510, 620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528, 647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 4
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Rhesus monkey
; US-11-010-874-4

Query Match 93.6%; Score 1442; DB 7; Length 339;
Best Local Similarity 93.1%; Pred. No. 2.5e-11; Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Db 338 TDSQKWEYCRIPSCSS 355

RESULT 11
US-11-010-874-8
; Sequence 8, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820_656
; CURRENT APPLICATION NUMBER: US/11/010, 874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963, 115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510, 620
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 8
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-010-874-8

Query Match 65.0%; Score 1001; DB 7; Length 168;
Best Local Similarity 99.4%; Pred. No. 1.5e-75; Mismatches 1; Indels 0; Gaps 0;
Matches 167; Conservative 0;

QY 88 CMHCSCENYDGSKISKTMGLECAQWDSQSOPHAGYIPS KFPNKNLCKNYCRNPDRRLPRW 147
Db 1 CMHCSCENYDGSKISKTMGLECAQWDSQSOPHAGYIPS KFPNKNLCKNYCRNPDRRLPRW 60

RESULT 13
US-11-010-874-13
; Sequence 13, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820_656
; CURRENT APPLICATION NUMBER: US/11/010, 874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963, 115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510, 620
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 13
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-010-874-13

Query Match 61.8%; Score 952; DB 7; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.5e-71; Mismatches 0; Indels 0; Gaps 0;
Matches 160; Conservative 0;

QY 6 CKTGNGKNGYRGTMSKTKNGTICKQNSSTSPPRSPATPSEGLENYCNPNDPQGP 65
Db 1 CKTGNGKNGYRGTMSKTKNGTICKQNSSTSPPRSPATPSEGLENYCNPNDPQGP 60

RESULT 12
US-11-010-874-9
; Sequence 9, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820_656
; CURRENT APPLICATION NUMBER: US/11/010, 874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963, 115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510, 620
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Rhesus monkey
; US-11-010-874-9

Query Match 61.9%; Score 954; DB 7; Length 168;
Best Local Similarity 94.6%; Pred. No. 1.1e-71; Mismatches 5; Indels 0; Gaps 0;

QY 88 CMHCSCENYDGSKISKTMGLECAQWDSQSOPHAGYIPS KFPNKNLCKNYCRNPDRRLPRW 147
Db 1 CMHCSCENYDGSKISKTMGLECAQWDSQSOPHAGYIPS KFPNKNLCKNYCRNPDRRLPRW 60

RESULT 14
US-11-010-874-14
; Sequence 14, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820_656
; CURRENT APPLICATION NUMBER: US/11/010, 874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963, 115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510, 620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528, 647
; PRIOR FILING DATE: 2003-12-11

```

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Rhesus monkey
; US-11-010-874-14

Query Match      58.2%; Score 896; DB 7; Length 160;
Best Local Similarity 93.8%; Pred. No. 5.7e-67; Mismatches 6; Indels 0; Gaps 0;
Matches 150; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy   6 CTKTGNGKNYGTGMSKTKNGTCKQKSSTSPPRSPATPSEGMENTCRNPNDPQGP 65
Db   1 CTKTGNGKNYGTGMSKTKNGTCKQKSSTSPPRSPATPSEGLENLYCRNPNDPQGP 60
Qy   66 WCYTDPPEKRDYCDTLCBECMHSGENIDGKISKTMGGLECOAWDSOPHANGIIPS 125
Db   61 WCYTDPPEKRDYCDTLCBECMHSGENIDGKISKTMGGLECOAWDSOPHANGIIPS 120
Qy   126 KFPNKLKKNCRNPDEPRWCFTTDPNKWLCDIPRC 165
Db   121 KFPNKLKKNCRNPDEPRWCFTTDPNKWLCDIPRC 160

RESULT 15
US-11-010-874-10
; Sequence 10, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FILE REFERENCE: 5820_656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 168
; TYPE: PRT
; ORGANISM: porcine
; US-11-010-874-10

Query Match      57.3%; Score 883; DB 7; Length 168;
Best Local Similarity 84.5%; Pred. No. 6.9e-65; Mismatches 12; Indels 0; Gaps 0;
Matches 142; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Qy   88 CHMCSGENYDGKISKTMGSLCQAMDSOPHANGIIPSKPKNLKKNYCRNPDRLRPW 147
Db   1 CMHCSGHRYEGKISKTMGSLCQAMDSOPHANGIIPSKPKNLKKNYCRNPDRLRPW 60
Qy   148 CPTIDPNKRLWELCDIPRCTTPPSSGGPYQCJKGTCYGNVRAVTSGHTQOHWSAQTP 207
Db   61 CPTIDPNKRGWECFCDIPRCTTPPSSGGPYQCJKGTCYGNVRAVTSGHTQOHWSAQTP 120
Qy   208 HTHERTPENFPCKNLDERYCRRNPGKRPWCHTNNSOVRWETCKIPSC 255
Db   121 HKHNRTPENFPCKNLDENYCRNPDGTAFWCYTIDSEVRWMDYCKIPSC 168

```

Search completed: January 25, 2006, 17:22:35
 Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 25, 2006, 17:01:00 ; Search time 161 Seconds

US-09-502-176-2
Perfect score: 1540

Sequence: I VYLS ECKTGNGK NYRGTM SK: TNSQ VRMEV YCKI PSCD SSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05-80:
1: uniprot_sprot:
2: uniprot_trembl:
SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	1535	99.7	PLMN_HUMAN	P00747 homo sapien
2	1535	99.7	PLMN_HUMAN	Q5teh1 homo sapien
3	1458	99.7	PLMN_BOVIN	Q5R8X6 pongo pygmaeus
4	1442	93.6	PLMN_MACMU	P12545 macaca mulatta
5	1306	84.8	PLMN_CANFIA	Q8wmrl canis familiaris
6	1299	84.4	PLMN_RAT	Q5BKB6 rattus norvegicus
7	1299	84.4	Q5BKB6_RAT	rattus norvegicus
8	1292	83.9	PLMN_PIG	P06867 sus scrofa
9	1291	83.8	PLMN_BOVIN	P06868 bos taurus
10	1279	83.1	Q5TCIO_MOUSE	O6tcio mus musculus
11	1279	83.1	PLMN_MOUSE	P20918 mus musculus
12	1237	80.3	PLMN_BIEBU	P029495 erinaceus europaeus
13	1203.5	78.1	Q5TPB4_RAT	07tpb4 rattus norvegicus
14	1160	75.3	PLMN_MACEU	P018793 macrocebus eu
15	996	64.7	Q5PBA6_BRAR3	Q5pb6 brachyrhynchus
16	962	62.5	Q5OLG6_ORYIA	O50196 oryza latifolia
17	959	62.3	Q5DVP8_ONCMI	Q5dvp8 oncorhynchus
18	881	57.2	Q5B992_ERIEU	Q5b992 erinaceus europaeus
19	809.5	52.6	Q5GP14_XENLA	Q5gp14 xenopus laevis
20	809.5	52.6	Q51691_XENLA	Q51691 xenopus laevis
21	797	51.8	HCP_HUMAN	P14210 homo sapiens
22	796	51.7	Q5ZTN9_XENLA	Q5ztn9 xenopus laevis
23	795.5	51.7	P07006_XENLA	P70006 xenopus laevis
24	782	50.8	HCP_RAT	P17915 rattus norvegicus
25	778	50.5	Q5P978_CHICK	Q5p978 gallus gallus
26	778	50.5	Q567B7_CANFA	Q567b7 canis familiaris
27	777	50.5	Q5C956_MOUSE	Q5c956 mus musculus
28	776.5	50.4	Q01402_9PIPI	Q01402 xenopus laevis
29	776	50.4	HCP_MOUSE	Q08048 mus musculus
30	776	50.4	Q53W55_MOUSE	Q53w55 mus musculus
31	730	2	Q76BS1_BOVIN	Q76bs1 bovis taurinus

ALIGNMENTS

RESULT 1	ID	PLMN_HUMAN	STANDARD;	PRT;	810 AA.
PLMN_HUMAN	P00747; Q51M46; Q6P00;	PLMN_HUMAN	AC	DT	01-MAR-1989 (Rel. 01, Created)
	21-JUN-1986 (Rel. 01, Last sequence update)		DT	13-SEP-2005 (Rel. 48, Last annotation update)	
			DE		Plasminogen precursor (EC 3.4.21.7) [Contains]
			DE		Activation peptide; Angiotatin; Plasmin heavy chain A, short form;
			DE		Plasmin light chain B).
			GN		Name=PLG;
			OS		Homo sapiens (Human).
			OC		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			OC		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
			OX		Hominoidea; Hominidae;
			RN		[1] NCBI_TaxID=9606;
			RN		NUCLEOTIDE SEQUENCE, AND VARIANT ASN-472.
			RX		NUCLEOTIDE SEQUENCE.
			RX		MEDLINE=90202879; PubMed=2318848;
			RA		Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
			RT		"Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system.";
			RT		J. Biol. Chem. 265:6104-6111(1990).
			RL		[2] NUCLEOTIDE SEQUENCE.
			RL		MEDLINE=90202879; PubMed=2318848;
			RN		Forbgen M., Raden B., Israelsson M., Larsson K., Heden L.-O.;
			RN		"Molecular cloning and characterization of a full-length cDNA clone for human plasminogen.";
			RN		PLoS Biol. 2005;3(4):e117.
			RL		PLBS Lett. 213:254-260 (1987).
			RN		[3] NUCLEOTIDE SEQUENCE.
			RN		TISSUE=Liver;
			RC		RCBrowne M.J., Chapman C.G., Dodd I., Carey J.B., Lawrence G.M.P.,
			RA		Mitchell D., Robinson J.H.;
			RA		"Expression of recombinant human plasminogen and aglycoplasmogen in HeLa cells";
			RA		Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
			RA		[4] NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS LYS-57; GLN-133; RPR HIS-261; TRP-408; ASN-472; VAL-494 AND TRP-523.
			RR		RR HIS-261; TRP-408; ASN-472; VAL-494 AND TRP-523.
			RR		Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
			RR		"SeattleSeqs. NHBLI HL64682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)." ;
			RR		Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
			RR		[5] NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].
			RR		TISSUE=Kidney;
			RR		MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
			RA		Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
			RA		Klauber R.D., Collins F.S., Wagner L., Sheehan C.M., Schuler G.D.,
			RA		Altshuler S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
			RA		Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

- RA Diatchenko L., Marukina K., Farmer A.A., Rubin G.M., Hong L., Hong L., Schetetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiro P., Carnicci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiro P., Carnicci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahy S.J., RA Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A., RA Fabey J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., RA Schnorr A., Schein J.E., Jones S.J.M., Marra M.A.; RA "Generation and initial analysis of more than 15,000 full-length human RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)."
- [6] PROTEIN SEQUENCE OF 20-810, AND VARIANT ASN-472.
RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;
RL submitted (JUL-1977) to the PIR data bank.
- [7] NUCLEOTIDE SEQUENCE OF 292-810.
RX MEDLINE=85023311; PubMed=6148961;
- [8] PROTEIN SEQUENCE OF 20-100.
RX MEDLINE=85093329; PubMed=1229312;
- [9] PROTEIN SEQUENCE OF 95-580; PubMed=581-626; 657-700 AND 732-810, AND VARIANT ASN-472.
RT "Structural relationship between 'glutamic acid' and 'lysine' forms of human and bovine plasminogen.";
RT activation peptide as studied by affinity chromatography.";
RL Biochemistry 23:4243-4250(1984).
- [10] PROTEIN SEQUENCE OF 483-604.
RX MEDLINE=76033692; PubMed=1268663;
- [11] PROTEIN SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
- [12] ACTIVE SITE.
RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
RL "The primary structure of human plasmin. II. The histidine loop of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
- [13] ACTIVE SITE.
RA MEDLINE=6924739; PubMed=4240117;
- [14] OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX Grosskopf W.R., Summaria L., Robbins K.C.;
"Studies on the active center of human plasmin. Partial amino acid sequence of a peptide containing the active center serine residue.";
J. Biol. Chem. 244:3590-3597(1969).
- [15] FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RA MEDLINE=85054794; PubMed=6094526;
- [16] PHOSPHORYLATION SITE SER-597.
RX MEDLINE=88185329; PubMed=9201958; DOI=10.1021/bi970328d;
- [17] CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=98185329; PubMed=3366193;
- [18] CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441; DOI=10.1074/jbc.272.11.7408;
- [19] CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=95042778; PubMed=7525077; DOI=10.1056/0052-8674(94)90200-3;
- [20] CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=9238710; PubMed=9102221;
- [21] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=93031502; PubMed=1657148;
- [22] X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=9231503; PubMed=1657149;
- [23] X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RX MEDLINE=1529951; DOI=10.1107/S09074496012267;
- [24] "Cryystal and molecular structure of human plasminogen kingle 4 refined at 1.9-A resolution.";
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulchak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of human plasminogen kingle 4.";
RL Biochemistry 30:10587-10598(1991).
- [25] X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RX MEDLINE=9231503; PubMed=1657149;
- [26] "Structure of human plasminogen kingle 4 at 1.68 Angstrom and 277 K. A possible structural role of disordered residues.";
RL Acta Crystallogr. D 53:169-178(1997).

RN [24] CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
 RP X-RAY

Query Match 99.7%; Score 1535; DB 1; Length 810;
 Best Local Similarity 99.6%; Pred. No. 2.4e-108;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLESECKTGNGKNGYRGTMSTKNGITCOKWSTSSPHRPRFSPATHPSBGLENYCRNPDN 60
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00114; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00115; TRYPSIN_SER; 1.

QY 98 VVLESECKTGNGKNGYRGTMSTKNGITCOKWSTSSPHRPRFSPATHPSBGLENYCRNPDN 157
 DR KW Hydrolase; Kringle; Protease; Repeat; Serine protease.
 DR SEQUENCE 810 AA; 90569 MW; 8B3ICB87/CCB3A6 CRC64;

Query Match 99.7%; Score 1535; DB 2; Length 810;
 Best Local Similarity 99.6%; Pred. No. 2.4e-108;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 61 DPGQPCWYCTTDPEKKRYVCDLCEBBMHCMSGENYTGKISKIMSGLRCQWDSDSPHAK 120
 DR 158 DPGQPCWYCTTDPEKKRYVCDLCEBBMHCMSGENYTGKISKIMSGLRCQWDSDSPHAK 217
 DR PROSITE; PS00115; TRYPSIN_HIS; UNKNOWN_1.
 DR KW Hydrolase; Kringle; Protease; Repeat; Serine protease.
 DR SEQUENCE 810 AA; 90569 MW; 8B3ICB87/CCB3A6 CRC64;

QY 121 GYPSKEPKNOKLKGKNCYRNPDRLPWCFTDPNPKWELCDIPRCTTPPPSSGPTVCLK 180
 DR 218 GYPSKEPKNOKLKGKNCYRNPDRLPWCFTDPNPKWELCDIPRCTTPPPSSGPTVCLK 277
 DR PROSITE; PS00115; TRYPSIN_HIS; UNKNOWN_1.
 DR KW Hydrolase; Kringle; Protease; Repeat; Serine protease.
 DR SEQUENCE 810 AA; 90569 MW; 8B3ICB87/CCB3A6 CRC64;

QY 181 GTGENTFRGNVAVTVSGTCOMSAQTPHTHTPENPCKOLDENTCRNPDKRAFWCHT 240
 DR 278 GTGENTFRGNVAVTVSGTCOMSAQTPHTHTPENPCKOLDENTCRNPDKRAFWCHT 337
 DR PROSITE; PS00115; TRYPSIN_HIS; UNKNOWN_1.
 DR KW Hydrolase; Kringle; Protease; Repeat; Serine protease.
 DR SEQUENCE 810 AA; 90569 MW; 8B3ICB87/CCB3A6 CRC64;

Db 241 TNSQVRWEYCKIPSCDSSPV 260
 DR 218 GYPSKEPKNOKLKGKNCYRNPDRLPWCFTDPNPKWELCDIPRCTTPPPSSGPTVCLK 277
 DR PROSITE; PS00115; TRYPSIN_HIS; UNKNOWN_1.
 DR KW Hydrolase; Kringle; Protease; Repeat; Serine protease.
 DR SEQUENCE 810 AA; 90569 MW; 8B3ICB87/CCB3A6 CRC64;

Db 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 2

QSTER4 HUMAN PRELIMINARY; PRT; 810 AA.

ID QSTER4; Human Preliminary; PRT; 810 AA.

AC QSTER4;

DT 01-FEB-2005 (TREMBLrel. 29, Created)

DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)

DR Plasminogen; Homo_sapiens (Human); Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchoptoglires; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

GN [1] NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.

RA Tracey A.; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

RL EMBL; AL109933; CAI22908.1; -; Genomic_DNA.

DR SMR; QSTER4; 563-810.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0004283; F:plasmin activity; IEA.

DR GO; GO:003809; F:thrombin activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:007595; F:blood coagulation; IEA.

DR GO; GO:0050874; F:organismal physiological process; IEA.

DR GO; GO:0005058; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR00314; PAN.

DR InterPro; IPR003609; Pan app.

DR InterPro; IPR011358; PepT_SIA_Plasm.

DR InterPro; IPR001254; Peptidase_S1_S6.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR003966; Peptidase_S1A_pr.

DR Pfam; PF00051; Kringle; 5.

DR Pfam; PF00024; PAN; 1.

DR Pfam; PF00089; Trypsin; 1.

DR PIRSF; PIRSF001150; Plasmin; 1.

DR PRINTS; PR00072; CHYMOTRYPSIN.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR003966; Peptidase_S1A_pr.

DR SMART; SM00130; KR; 5.

DR SMART; SM00473; PAN_AP; 1.

DR SMART; SM00020; Tryp_SPC; 1.

RESULT 3

Q5R8X6_PONY PRELIMINARY; PRT; 810 AA.

ID Q5R8X6; PONY PRELIMINARY; PRT; 810 AA.

AC Q5R8X6;

DT 01-FEB-2005 (TREMBLrel. 29, Created)

DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)

DR Plasminogen; Homo_sapiens (Human); Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchoptoglires; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9600;

GN [1] NUCLEOTIDE SEQUENCE.

OC Pongo_pygmaeus (Orangutan); Buarchoptoglires; Primates; Catarrhini; Hominidae; Mammalia; Butheria; Buarchoptoglires; Primates; Catarrhini; Hominidae; Pongo.

DR TISSUE=Liver;

DR The German cDNA Consortium; The German cDNA Consortium; Poustka A., Albert R., Moosmayer P., Schupp J., Wellenreuther R., RA Newes H.W., Weil B., Amid C., Osanger A., Bobo G., Han M., Wiemann S.; Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR855622; CAH91784.1; -; mRNA.

DR SMR; Q5R8X6; 195-352; 564-810.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:000233; F:peptidase activity; IEA.

DR GO; GO:0004283; F:plasmin activity; IEA.

DR GO; GO:003809; F:thrombin activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:007595; F:blood coagulation; IEA.

DR GO; GO:0050874; F:organismal physiological process; IEA.

DR GO; GO:0005058; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR001314; PAN.

DR InterPro; IPR003966; Peptidase_S1_S6.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR003966; Peptidase_S1A_pr.

DR SMART; SM00130; KR; 5.

DR SMART; SM00473; PAN_AP; 1.

DR PIRSF; PIRSF001150; Plasmin; 1.

DR PRINTS; PR00072; CHYMOTRYPSIN.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR003966; Peptidase_S1A_pr.

DR SMART; SM00020; Tryp_SPC; 1.

DR	Pfam; PF00051; Kringle; 5.	CC	collagenases and several complement zymogens, such as C1 and C5.
DR	Pfam; PF00024; PAN; 1.	CC	It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
DR	Pfam; PF00089; Trypsin; 1.	CC	-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-1-Xaa > Arg-1-Xaa;
DR	PIRF; PIREF001150; Plasmin; 1.	CC	higher selectivity than trypsin. Converts fibrin into soluble products.
DR	PRINTS; PRO0722; CHIOTRYPsin.	CC	-!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Activated with catalytic amounts of streptokinase.
DR	PRINTS; PRO0018; KRINGLE.	CC	-!- SUBCELLULAR LOCATION: Secreted.
DR	PRINTS; PRO1505; PROTHROMBIN.	CC	-!- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-580, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
DR	PROBOM; PD000395; Kringle; 5.	CC	-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
DR	SMART; SM00130; KR; 5.	CC	-!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.
DR	SMART; SM00433; PAN_AP; 1.	CC	-!- SIMILARITY: Contains 5 kringle domains.
DR	SMART; SM00202; TRYSPC; 1.	CC	-!- SIMILARITY: Contains 1 PAN domain.
KW	Hydrolase; Hypothetical protein; Kringle; Protease; Repeat; Serine protease.	CC	-!- SIMILARITY: Contains 1 peptidase S1 domain.
SEQUENCE	SO 810 AA; 90380 MW; 126D530C942ADD4 CRC64;	CC	-----
Query	Match 94.7%; Score 1458; DB 2; Length 810;	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its contents is in no way modified and this statement is not removed.
QY	Best Local Similarity 95.0%; Pred. No. 1. 7e-102; Mismatches 10; Indels 0; Gaps 0;	CC	-----
QY	1 VYLSECKTGNKGNYRGMSKTRGKTCQKWSSTSPHRPRFPAHSEGLEYCRNPDN 60	CC	DR EMBL; J06697; AA34901.1; -; mRNA.
Db	98 YLSECKTGNKGNYRGMSKTRGKTCQKWSSTSPHRPRFPAHSEGLEYCRNPDN 157	CC	DR FIR; B32869; B30848.
QY	61 DPGKCYTTDEKRKYCDLRCERCHCMHSGENTDGKTSKTMSCLEQWDSOPHAH 120	CC	DR HSSP; P00747; IBIU.
Db	158 DAQGPWCYTDPHEVYDCDIPCEBACMHSGENYGKISTKTMSCLEQWDSOPHAH 217	CC	DR SMR; P12545; 184-352; 564-810.
QY	121 GTPSKPKPNKLNKNTKRNPKDPLRPPCFTDPNPKMLCDIPRCCTPPSSGPTVQCK 180	CC	DR MEROPS; S01.233; -.
Db	218 GTPSKPKPNKLNKNTKRNPKDPLRPPCFTDPNPKMLCDIPRCCTPPSSGPTVQCK 277	CC	DR InterPro; IPRO00001; Kringle.
QY	181 GIGENYGRGNVAVTGSHTCQHSAQTPTHTERTPENPKCKLDENTCRNPDKGRAPWHT 240	CC	DR InterPro; IPRO03014; PAN.
Db	278 GGTENYGRGNVAVTGSHTCQHSAQTPTHTERTPENPKCKLDENTCRNPDKGRAPWHT 337	CC	DR InterPro; IPRO03609; Pan_APP.
QY	241 TNSQVRWEYCKIPSCGSSPV 260	CC	DR InterPro; IPRO01138; Peptidase_S1_S6.
Db	338 TNSQVRWEYCKIPSCGSSPV 357	CC	DR InterPro; IPRO01314; Peptidase_SIA.
RESULT 4	PLMN_MACMU ID PLMN_MACMU STANDARD; PRT; 810 AA.	CC	DR InterPro; IPRO03966; Peptidase_SIA_Pr.
AC	P12545; 01-OCT-1989 (Rel. 1.2, Created)	CC	DR Pfam; PF00051; Kringle; 5.
DT	01-OCT-1989 (Rel. 1.2, Last sequence update)	CC	DR Pfam; PF00024; PAN; 1.
DT	13-SEP-2005 (Rel. 4.8, Last annotation update)	CC	DR Pfam; PF00089; Trypsin; 1.
DR	Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Plasmin heavy chain A; Activation peptide, Plasmin heavy chain A; Activation peptide, Plasmin light chain B].	CC	DR PRINTS; PRO0722; CHIOTRYPsin.
DB	Macaca mulatta (Rhesus macaque). Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca. NCBI TaxID=5544; MEDLINE=89144660; PubMed=22925643; Tomlinson, J.E., McLean, J.W., Lawn, R.M.; "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.", J. Biol. Chem., 264:5957-5965 (1989). FUNCTION: plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator.	CC	DR PRINTS; PRO1505; PROTHROMBIN.
RN	[1] NUCLEOTIDE SEQUENCE.	CC	DR PROBOM; PD000395; Kringle; 5.
RR	MEDLINE=89144660; PubMed=22925643; Tomlinson, J.E., McLean, J.W., Lawn, R.M.; "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.", J. Biol. Chem., 264:5957-5965 (1989). FUNCTION: plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator.	CC	DR SMART; SM00130; KR; 5.
FT	CHAIN SIGNAL 1 19	CC	DR SMART; SM00433; PAN_AP; 1.
FT	CHAIN 20 810	CC	DR SMART; SM00202; TRYSPC; 1.
FT	CHAIN 20 580	CC	DR PROBOM; PD000395; Kringle; 5.
FT	PEPTIDE 20 96	CC	DR SMART; SM00133; TRYPSIN_HIS; 1.
FT	CHAIN 97 580	CC	DR PROBOM; PD000395; Kringle; 5.
FT	CHAIN 581 810	CC	DR PROBOM; PD000395; Kringle; 5.
FT	DOMAIN 20 98	CC	DR PROBOM; PD000395; Kringle; 5.
FT	DOMAIN 103 181	CC	DR DOMAIN 184 262
FT	DOMAIN 275 352	CC	DR DOMAIN 275 352
FT	DOMAIN 377 454	CC	DR DOMAIN 377 454

FT DOMAIN 481 560 Kringle 5.
 FT DOMAIN 581 808 Peptidase sl.
 FT ACT_SITE 622 Charge relay system.
 FT ACT_SITE 665 665 Charge relay system.
 FT ACT_SITE 760 Charge relay system.
 FT BINDING 134 134 Fibrin.
 FT BINDING 136 136 Fibrin.
 FT BINDING 158 158 Omega-aminocarboxylic acids.
 FT BINDING 172 172 Omega-aminocarboxylic acids.
 FT BINDING 432 432 Omega-aminocarboxylic acids.
 FT BINDING 445 445 Omega aminocarboxylic acids. O-linked (GalNAc. .) (By similarity).
 FT CARBOHYD 365 365 O-linked (GalNAc. .) (By similarity).
 FT DISURFID 49 73 By similarity.
 FT DISURFID 53 61 By similarity.
 FT DISURFID 103 181 By similarity.
 FT DISURFID 124 164 By similarity.
 FT DISURFID 152 176 By similarity.
 FT DISURFID 185 262 By similarity.
 FT DISURFID 188 316 By similarity.
 FT DISURFID 205 245 By similarity.
 FT DISURFID 234 257 By similarity.
 FT DISURFID 275 352 By similarity.
 FT DISURFID 295 335 By similarity.
 FT DISURFID 324 347 By similarity.
 FT DISURFID 377 454 By similarity.
 FT DISURFID 398 437 By similarity.
 FT DISURFID 426 449 By similarity.
 FT DISURFID 481 560 By similarity.
 FT DISURFID 502 543 By similarity.
 FT DISURFID 531 555 By similarity.
 FT DISURFID 567 685 Interchain (between A and B chains) (By similarity).
 FT DISURFID 577 585 Interchain (between A and B chains) (By similarity).
 FT DISURFID 607 623 By similarity.
 FT DISURFID 699 766 By similarity.
 FT DISURFID 729 745 By similarity.
 FT DISURFID 755 784 By similarity.
 SQ SEQUENCE 810 AA; 90255 MW; A75EIC51AIA0P24A CRC64;

Query Match 93.6%; Score 1442; DB 1; Length 810;
 Best Local Similarity 93.1%; Pred. No. 2.8e-101; Gaps 0; Matches 242; Conservative 9; Mismatches 9; Indels 0; Gap 0;

QY 1 VYLSECKTGKNGKRYGTMKTKNGTQKWAESTSPHRPRESPATRSEGLENYCNPNDN 60
 Db 98 VYLSECKTGKNGKRYGTMKTKNGTQKWAESTSPHRPRESPATRSEGLENYCNPNDN 157

QY 61 DPGGPWCTTPEKRYDTCDFLCECBOMHSGENYDGKSKRTMMSGLEQWADSDOPHAH 120
 Db 158 DPGGPWCTTPEKRYDTCDFLCECBOMHSGENYDGKSKRTMMSGLEQWADSDOPHAH 217

QY 121 GYIPSKEPNPKULKKNYCRNPRLPWCFTDPNPKWELCIPRCCTPPSSGPTQYICK 180
 Db 218 GYIPSKEPNPKULKKNYCRNPRLPWCFTDPNPKWELCIPRCCTPPSSGPTQYICK 277

QY 181 GTGENYTRGNVAVTVSHTCQMSAQPTHTPENPPCKNLDENYCRNPDKRAPWHT 240
 Db 278 GYGENTRGNVAVTVSHTCQMSAQPTHTPENPPCKNLDENYCRNPDKRAPWHT 337

RESULT 5
 ID 08WMRI_CANFA
 ID 08WMRI_CANFA PRELIMINARY; PRT; 359 AA.
 Db 338 TNSQVRWEYCKIPSCSSPV 357

RESULT 6
 PLMN_RAT ID PLMN_RAT STANDARD; PRT; 812 AA.
 AC Q01177; Q0ROW3; (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 48, Last annotation update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) (Contains: Plasmin heavy chain A; Activation Peptide; Angiotatin; Plasmin heavy chain A, short form; DE Plasmin light chain B).

DB Plasminogen (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis
 NCBI_TAXID=9615;
 RN [1]
 RPP NUCLEOTIDE SEQUENCE.
 RA Pirle-Shephard S.R.; Coffman K.T.; Resnick D.; Chan R.; Kisker O.; Folkman J.; Waters D.J.; Submitted (DEC-2001) to the EMBL/GenBank/DDJB databases.
 RRL EMBL; AY059985; AAI58519.1; -; mRNA.
 DR HSSP; P00147; 1PMK.
 DR SMR; 08WMRI; 87-255.
 DR Ensemble; ENSCAFG00000000759; Canis familiaris.
 DR GO; GO:0055050; F:calcium ion binding; IEA.
 DR GO; GO:0003809; P:thrombin activity; IEA.
 DR GO; GO:0007591; P:blood coagulation; IEA.
 DR InterPro; IPR000001; Kringle.
 DR IntraPro; IPR003965; Peptidase_SIA_pr.
 DR Pfam; PF00051; Kringle_4.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; P000335; Kringle_4.
 DR SMART; SM00130; KR_4.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS50070; KRINGLE_2; 4.
 DR KW Kringle.
 FT NON_TER 359 1
 FT NON_TER 359 359
 SQ SEQUENCE 359 AA; 41172 MW; 776D35P4AB0BDD9B CRC64;

Query Match 84.8%; Score 1306; DB 2; Length 359;
 Best Local Similarity 81.2%; Pred. No. 2.6e-91; Matches 211; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKRYGTMKTKNGTQKWAESTSPHRPRESPATRSEGLENYCNPNDN 60
 Db 1 VYLSECKTGKNGKRYGTMKTKNGTQKWAESTSPHRPRESPATRSEGLENYCNPNDN 60

QY 61 DPGGPWCTTPEKRYDTCDFLCECBOMHSGENYDGKSKRTMMSGLEQWADSDOPHAH 120
 Db 61 DPGGPWCTTPEKRYDTCDFLCECBOMHSGENYDGKSKRTMMSGLEQWADSDOPHAH 120

QY 121 GYIPSKEPNPKULKKNYCRNPRLPWCFTDPNPKWELCIPRCCTPPSSGPTQYICK 180
 Db 121 GYIPSKEPNPKULKKNYCRNPRLPWCFTDPNPKWELCIPRCCTPPSSGPTQYICK 180

QY 181 GTGENYTRGNVAVTVSHTCQMSAQPTHTPENPPCKNLDENYCRNPDKRAPWHT 240
 Db 181 GTGENYTRGNVAVTVSHTCQMSAQPTHTPENPPCKNLDENYCRNPDKRAPWHT 240

QY 241 TNSQVRWEYCKIPSCSSPV 260
 Db 241 TNSQVRWEYCKIPSCSSPV 260

Db 241 TNSEVRWEHCOLPSCSPI 260

OX NCBI_TaxID=10116;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Bartelt K., Johnsen A.H., Thorsten S.;
 RT "Rat plasminogen: cDNA and gene structure.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE OF 343-511.
 RX TISSUE=Liver; PubMed=1645711;
 MEDLINE=91250378;
 RA Kanalas J.J., Makker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (gp330) as a receptor site for plasminogen";
 RL J. Biol. Chem. 266:10825-10828(1991).
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
 CC -!- FUNCTION: Angiotatin is an angiogenesis inhibitor that blocks neovascularization and growth of experimental primary and metastatic tumors in vivo (By similarity).
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PMW: In the presence of the inhibitor, the activation involves only cleavage after Arg-581, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.
 CC -!- SIMILARITY: Contains 5 kringle domains.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.

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EMBL: AJ242649; CAB46014.1; -; mRNA.
 EMBL: M62832; AAH41884.1; -; mRNA.
 PIR: A40522; A40522.
 DR P00477; 1PIRK.
 DR SNR; Q01177; 565-812.
 DR MEROPS; S01_233; -; Rattus norvegicus.
 DR EMBL; ENSRNOG0000017223; Rattus norvegicus.
 DR RGD; 619893; PIG.
 DR InterPro; IPR00001; Kringle.
 DR InterPro; IPR03014; PAN.
 DR InterPro; IPR00509; Pan app.
 DR InterPro; IPR011358; Pept_SIA_Plasm.
 DR InterPro; IPR01254; PeptTable_S1_S6.
 DR InterPro; IPR01314; Peptidase_SIA.
 DR InterPro; IPR003966; Peptidase_SIA_pr.
 DR Pfam; PF00051; Kringle_5.
 DR Pfam; PF00054; PAN_1.
 DR Pfam; PF00059; Trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRRINGLE.

DR PRINTS; PRO1505; PROTHROMBIN.
 DR PRODom; PD000395; Kringle_1.
 DR SMART; SM00130; KR_1.
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 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; FibrinoLyse; Hydrolase; Kringle; Plasma; protease; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 KW SIGNAL 1 19
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 FT CHAIN 20 581 19
 FT PEPTIDE 20 97 19
 FT CHAIN 98 581 19
 FT DOMAIN 98 246 19
 FT DOMAIN 582 812 19
 FT DOMAIN 20 98 19
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 FT DOMAIN 184 262 19
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 FT DISULFID 206 245 19
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 FT CONFLICT 418 418 19
 FT SEQUENCE 812 AA; 90536 MW; 8C703C51410BBC9B CRC64;

Query Match 1 84.4%; Score 1299; DB 1; Length 812;
 Best Local Similarity 82.6%; Pred. No. 2,1e-90; Indels 0; Gaps 0;
 Matches 213; Conservative 21; Mismatches 24; Identity 1.

Qy 1 VVLSCEKTGNGKVKYRTMSKTKNGTCKQKSSTSPHRPRESPAATHPSEGRLNEYCRNPDN 60
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Qy 61 DPGQPMKTYITDPEKRYDQDILACERCMHCSEGENYDGKSKTMSSGLCQWADSQPHH 120
 Db 158 DPGQPMKTYITDPEKRYDQDILACERCMHCSEGENYDGKSKTMSSGLCQWADSQPHH 217

Qy 121 GTPSKPKNPKLKKNTCRNPDRRELWPCTTDPNKKGWELCDIPRCMTTPPSGGPTVQCLK 180

Db 218 GTPAKPKPSKQKMKNCRNPPDGPBPWCFITDPNKEWYCDIPRCMTTPPPGPTVQCLK 277

QY 181 GTGENTRGNVAVTWSHTCWSAQPHTHERTPENPCKDUDENYCRNPGKRAPWCHT 240
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 DR PRINTS; PRO0018; KRINGLE.
 DR PRINTS; PRO1505; PROTHROMBIN.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN AP; 1.
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 Name=PIG;
 OS Rattus norvegicus (Rat).
 OC BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
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 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=21388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
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 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bustow K.H., Schaffer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
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 RA Bosak S.A., McEwan P.J., McKernan J.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Soergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinman J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.B.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Narra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA Sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RG NIH MGC Project;
 RL Submitted (Mar 2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011135; AAH91135.1; -; mRNA.
 DR GO: 0005509; F:calcium ion binding; IEA.
 DR GO: 0004263; F:chymotrypsin activity; IEA.
 DR GO: 0004283; F:plasmin activity; IEA.
 DR GO: 003388; F:fibrinolin activity; IEA.
 DR GO: 0004295; F:tryptsin activity; IEA.
 DR GO: 0007596; F:blood coagulation process; IEA.
 DR GO: 0050874; F:organismal physiological process; IEA.
 DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR00001; Kringle.
 DR InterPro; IPR00301; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR011358; Pept_SIA_Plasm.
 DR InterPro; IPR001254; PepTidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_SIA.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.

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 KW Hydrolase; Kringle; Protease; Repeat; Serine Protease.
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410BBC9B CRC64;
 Query Match 84.4%; Score 1299; DB 2; Length 812;
 Best Local Similarity 82.6%; Pred. No. 2.1e+90;
 Matches 213; Conservative 82.6%; Pred. No. 2.1e+90;
 Mismatches 24; Indels 0; Gaps 0;
 QY 1 VYLSECTKGNGKVRGTMSTKRGNTCKWSSTSPPRSPATPSGLBENYCRPDN 60
 DR 98 WLSECKTGIGKGYRQTMSTKGTGTCQKNSDTSPVPKSPSTHPSEGULBENYCRPDN 157
 QY 61 DPGQPCPYTTPEKEVYCDLICERECMCSGENTGKTSKTMSCLEQAWDSOPRAH 120
 DR 158 DBOGPWCPYTTDPDORYCYNTPCEBECMCSGKBYEKTSKTMSCLDOSWDOSPHAH 217
 DR 121 GYPSKEPNKOLKQKNCRNPDRLRWCFTDPKNEWLCDIPRCITPPPSGGPYCQLK 180
 DR 218 GYPAFEPKSKOLKQKNCRNPGCPEPRCPTPDKNEWLCDIPRCITPPPGPYCQLK 277
 DR 181 GTGENTRGNVAVTWSHTCWSAQPHTHERTPENPCKDUDENYCRNPGKRAPWCHT 240
 DR 278 GRGENTRGNVAVTWSHTCWSAQPHTHERTPENPCKDUDENYCRNPGKRAPWCHT 337
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 DR PROSITE; PS00135

RESULT 9	
PLMN	BOVIN
ID	- PLMN BOVIN STANDARD; PRT; 812 AA.
AC	P06868; Q28162;
DT	01-JAN-1988 (Rel. 06, Created) 01-NOV-1997 (Rel. 35, Last sequence update)
DE	Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Plasmin light chain B].
DB	Name=PIG;
GN	Bos taurus (Bovine).
OC	Bukaryota; Metazoa; Chordata; Crinata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC	Pecora; Bovidae; Bovinae; Bos.
OX	NCBI_TAXID=9113;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Liver; Berglund L., Andersen M.D., Petersen T.E.; "Cloning and characterization of the bovine plasminogen cDNA.", Int. Dairy J. 5:593-603 (1995).
RA	[2]
RL	PROTEIN SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
RN	MEDLINE=85203906; PubMed=3846532;
RA	Schallner J., Moser P.W., Dannegger-Muller G.A.K., Rosselot S.J., Kampfer U., Rickli E.B.; "Complete amino acid sequence of bovine plasminogen. Comparison with human plasminogen.", Eur. J. Biochem. 149:267-278 (1984).
RL	[3]
RP	NUCLEOTIDE SEQUENCE OF 706-812.
RX	MEDLINE=85023311; PubMed=6148961;
RA	Malinowski D.P., Sadler J.E., Davie E.W.; RT "Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.", Eur. J. Biochemistry 23:4243-4250 (1984).
RL	[4]
RP	CARBOHYDRATE-LINKAGE SITES.
RX	MEDLINE=88185329; PubMed=3356193;
RA	Martin T., Schallner J., Rickli E.B., Schmid K., Kamerling J.P., Gerwig G.J., van Halbeek H., Villegenthart J.F.; RT "The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns.", Eur. J. Biochem. 173:57-63 (1988).
RL	"The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns.", Eur. J. Biochem. 173:57-63 (1988).
CC	- I- PROTEOLYTIC ACTIVITY: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
CC	- I- CATALYTIC ACTIVITY: Preferential cleavage: Lys- Xaa > Arg- Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.
CC	- I- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
CC	- I- SUBCELLULAR LOCATION: Secreted.
CC	- I- PTM: N-linked glycan contains N-acetyl-lactosamine and sialic acid. O-linked glycans consist of Gal-GalNAc disaccharide which is modified with up to 2 sialic acid residues (microheterogeneity).
CC	- I- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-583, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
CC	- I- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
CC	- I- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC	subfamily.
CC	- I- SIMILARITY: Contains 5 kringle domains.
CC	- I- SIMILARITY: Contains 1 peptidase S1 domain.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL ou the European Bioinformatics Institute. There are no restriction to use as long as its content is in no way modified and this statement removed.
CC	EMBL: X79402; CAA5939.1; - ; mRNA.
CC	EMBL: K02935; AAA30714.1; - ; mRNA.
CC	PIR: S45056; PAN.
CC	DR IPRO03609; Pan app.
CC	DR InterPro; IPRO03609; Pept-SIA_Plasm.
CC	DR HSSP; P00747; 2PK4.
CC	DR SMR; P06868; 191-359, 568-812.
CC	DR MEROPS; S01.233; -.
CC	DR GlycositDB; P06868; -.
CC	DR InterPro; IPRO00001; Kringle.
CC	DR InterPro; IPRO003014; PAN.
CC	DR InterPro; IPRO01358; Pep-SIA_Plasm.
CC	DR InterPro; IPRO01254; Peptidase_S1_S6.
CC	DR InterPro; IPRO01314; Peptidase_SIA.
CC	DR InterPro; IPRO03966; Peptidase_SIA_Prot.
CC	DR Pfam; PF00024; PAN; 1.
CC	DR Pfam; PF00089; TRYPSIN; 1.
CC	DR PROSP; PIRSF001150; Plasmin; 1.
CC	DR PRINTS; PR00722; CHYMOTRYPSIN.
CC	DR PRINTS; PR00018; KRINGLE.
CC	DR PRINTS; PR01505; PROTHROMBIN.
CC	DR PROBOM; PDD00395; Kringle; 5.
CC	DR PROSITE; PS00021; KRINGLE_1; 5.
CC	DR PROSITE; PS50070; KRINGLE_2; 5.
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CC	DR PROSITE; PS50240; TRYPSIN_DOM; 1.
CC	DR PROSITE; PS00134; TRYPSIN_HIS; 1.
CC	KW Blood coagulation; Direct protein sequencing; Fibrinolysis; Glycoprotein; Hydrolase; Kringle; Plasma; Protease; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
CC	KW SIGNAL 1 26
FT	FT CHAIN 27 812
FT	FT DOMAIN 27 583
FT	FT PEPTIDE 27 104
FT	FT CHAIN 105 583
FT	FT DOMAIN 29 105
FT	FT DOMAIN 110 188
FT	FT DOMAIN 192 269
FT	FT DOMAIN 282 359
FT	FT DOMAIN 384 461
FT	FT DOMAIN 485 564
FT	FT DOMAIN 584 810
FT	FT DOMAIN 624 624
FT	FT ACT SITE 667 667
FT	FT ACT SITE 762 762
FT	FT ACT SITE 315 315
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FT	FT DISUFPID 60 68
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FT	FT DISUFPID 159 183
FT	FT DISUFPID 192 269
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FT	FT DISUFPID 584 810
FT	FT DISUFPID 624 624
FT	FT DISUFPID 667 667
FT	FT DISUFPID 762 762
FT	FT DISUFPID 810 810

- RA Nagaraja R.;
 RT "Genomic sequence analysis in the mouse t-complex region.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDJB databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Itohnyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquaiello N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holtky S.W.,
 RA Villanueva D.S., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E.,
 RA Schnerring A., Schein J.E., Jones J.S.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 1-16.
 RX STRAIN=129/SVJ; TISSUE=Liver;
 MEDLINE=22254843; PubMed=1214246; DOI=10.1074/jbc.M202509200;
 RA Barnach P.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
 RT "Localization of regulatory elements mediating constitutive and
 cytokine-stimulated plasminogen gene expression.";
 RL J. Biol. Chem. 277:8579-8588(2002).
 RN [5]
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0022-8674(94)90200-3;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.,
 RT "Angiotatin: a novel angiogenesis inhibitor that mediates the
 suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 CC !- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 a proteolytic factor in a variety of other processes including
 embryonic development, tissue remodeling, tumor invasion, and
 inflammation; it weakens the walls of the Graafian
 follicle. It activates the urokinase-type plasminogen activator,
 collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 Willebrand factor.
 CC !- FUNCTION: Angiotatin is an angiogenesis inhibitor that blocks
 metastatic tumors in vivo.
 CC !- CATALYTIC ACTIVITY: Preferential cleavage: Lys-| -Xaa > Arg-| -Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC !- ENZYME REGULATION: Converted into plasmin by plasminogen
 activators, both plasminogen and its activator being bound to
 fibrin. Cannot be activated with streptokinase.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- PTM: In the presence of the inhibitor, the activation involves
 only cleavage after Arg-501, yielding two chains held together by
 two disulfide bonds. In the absence of the inhibitor, the
 activation involves additionally the removal of the activation
 peptide (By similarity).
 CC !- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 immediately after dissociation from the clot.
 CC !- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 subfamily.
 CC !- SIMILARITY: Contains 5 kringle domains.
 CC !- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 EMBL; J04766; AA50168.1; -; mRNA.
 EMBL; AF491053; AAH22156.1; -; Genomic_DNA.
 EMBL; BC014773; AAH14773.1; -; mRNA.
 EMBL; BC057186; AAH7186.1; -; mRNA.
 EMBL; AX134430; AAH15805.1; -; Genomic_DNA.
 PIR; A3854; PLMS.
 HSSP; P00747; IBHU.
 SMR; P29318; 194-352, 566-812.
 MEROPS; S01.233; -.
 ENSMUSG00000055481; Mus musculus.
 MGI; MGI:97620; Plg.
 GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006915; P:apoptosis; IDA.
 GO; GO:006917; P:induction of apoptosis; IDA.
 DR GO; GO:0046716; P:muscle maintenance; IMP.
 GO; GO:0007519; P:negative regulation of angiogenesis; IMP.
 DR GO; GO:0016525; P:negative regulation of angiogenesis; TAS.
 DR GO; GO:0042246; P:tissue regeneration; IMP.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_SIA.
 DR InterPro; IPR0031966; Peptidase_SIA_pr.
 PFam; PF00051; Kringle_5.
 DR PFam; PF00024; PAN; 1.
 DR PFam; PF0089; Trypsin; 1.
 PIRSF; PIRSF001150; Plasmin; 1.
 PRINTS; PR00722; CHYNOTRIPSIN.
 DR PRINTS; PR00018; KRINGLE.
 PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; P000095; Kringle_5.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 PROSITE; PS50070; KRINGLE_2; 5.
 PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; direct_protein_sequencing; Fibrinolysis; Hydrolase;
 KW Tissue remodeling; Zymogen.
 FT SIGNAL 1 19
 FT CHAIN 20 812 Plasminogen.
 FT PEPTIDE 20 581 Plasmin heavy chain A.
 FT CHAIN 98 581 Activation peptide.
 FT CHAIN 98 97 Plasmin heavy chain A, short form.
 FT CHAIN 98 7436 Angiotatin.
 FT DOMAIN 582 812 Plasmin light chain B.
 FT DOMAIN 20 98 PAN.
 FT DOMAIN 103 181 Kringle 1.
 FT DOMAIN 184 262 Kringle 2.
 FT DOMAIN 275 352 Kringle 3.
 FT DOMAIN 377 454 Kringle 4.
 FT DOMAIN 481 560 Kringle 5.
 FT ACT SITE 624 624 Peptidase_S1.
 FT ACT SITE 667 667 Charge relay system (By similarity).
 FT ACT SITE 762 762 Charge relay system (By similarity).
 FT DISUFRID 49 73 By similarity.
 FT DISUFRID 53 61 By similarity.
 FT DISUFRID 103 181 By similarity.
 FT DISUFRID 124 164 By similarity.
 FT DISUFRID 152 176 By similarity.
 FT DISUFRID 185 By similarity.

FT DISULFID 188 316 By similarity.
 PT DISULFID 206 245 By similarity.
 FT DISULFID 234 257 By similarity.
 FT DISULFID 275 352 By similarity.
 FT DISULFID 296 335 By similarity.
 FT DISULFID 324 347 By similarity.
 FT DISULFID 377 454 By similarity.
 FT DISULFID 398 437 By similarity.
 FT DISULFID 426 449 By similarity.
 FT DISULFID 481 560 By similarity.
 FT DISULFID 502 543 By similarity.
 FT DISULFID 531 555 By similarity.
 FT DISULFID 568 687 By similarity (between A and B chains) (By similarity).
 FT DISULFID 578 586 By similarity (between A and B chains) (By similarity).
 FT DISULFID 609 625 By similarity.
 FT DISULFID 701 758 By similarity.
 FT DISULFID 731 747 By similarity.
 FT DISULFID 758 786 By similarity.
 FT CONFLICT 235 R -> H (in Ref. 1).
 FT CONFLICT 525 525 G -> D (in Ref. 1).
 FT CONFLICT 649 649 S -> L (in Ref. 1).
 SQ SEQUENCE 812 AA: 90782 MW: 2417326056A2FFD2 CRC64:
 Query Match Similarity 83.1%; Score 1279; DB 1; Length 812;
 Best Local Similarity 81.0%; Pire. No. 7-1e-89; Mismatches 22; Indels 0; Gaps 0;
 Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;
 Qy 1 VYLLERCKTQNGKNGYRGMISKTKGICQKWNSTSPHRPRESRATHPEGLERENYCRNPDN 60
 98 VYLLERCKTQNGKNGYRGMISKTKGICQKWNSTSPHRPRESRATHPEGLERENYCRNPDN 157
 Qy 61 DPGSQWVTTPEAKRYCDLCEBOMHSGENYDGKISKTMSLGECOWDSDOPAH 120
 158 DEQGPWVCTTPDPPDKRVDYCNCPTCCECMYSGKEKGKISKTMSLGECOWDSDOPAH 217
 Db 121 GYIPSKERNKNUKKNYCNRNPDRELRCMFTDPNKGMLCDIPRCTTPSSGGPTQCLK 180
 218 GYIPIKEPKSNKLKMYCNCRNPDPGEPRPFCITDPTPKWYCDIPRCTTPPPSPSPTQCLK 277
 Qy 181 GIGENRTRGNVAVTIVSGHTCQHSAQTETHTSRTPENPCKQDNLNTCRNPCKRAPWHT 240
 278 GRGENYRGTGTVSIVSGKNCORNSEQTPHRHRTPENPCKQDLENYCRNPQGETAPWCYT 337
 Db 241 TNSQVRMVKYKPSCDSS 258
 Qy 338 TDSQLRNEYCXPSCSES 355
 Db
 RESULT 12
 PLMN ERIEU
 ID PLMN_ERIEU STANDARD; PRT; 810 AA.
 AC 029485;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DB Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Plasmin heavy chain A, short form; Plasmin light chain B]
 DR Name=PLG;
 GN *Brinacoccus europaeus* (Western European hedgehog).
 OC Brinacoccus; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
 NCBI — TAXID:9365;
 RN [1] NUCLEOTIDE SEQUENCE.
 RC TISSUE:Liver;
 RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;
 RA Lawn R.M., Boomkamp N.W., Schwartz K., Wade D.P., Byrne C.D., Fong J.J., Meer J., Pattiy L.;
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of

RT hedgehog apolipoprotein(a)";
 RL J. Biol. Chem. 270:24004-24009 (1995).
 RL [2]
 RSEQUENCE REVISION.
 RA lawn R.M.; Submitted (PRB-1997) to the EMBL/GenBank/DDBJ databases.
 RL Submitter (PRB-1997)
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Lys-| -Xaa > Arg-| -Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.
 CC ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
 CC SUBCELLULAR LOCATION: Secreted.
 CC PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-582, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
 CC MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
 CC SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.
 CC SIMILARITY: Contains 5 kringle domains.
 CC SIMILARITY: Contains 1 PAN domain.
 CC SIMILARITY: Contains 1 peptidase S1 domain.
 DR EMBL: U33171; AAC48717.1; mRNA.
 DR PIR: I46260; I46260.
 DR HSSP: P00747; IBSI.
 DR SMR; Q29485; 568-810.
 DR MEROPS; S01.233; -
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan.app.
 DR InterPro: IPR011358; Pept.SIA_Plasmin.
 DR InterPro: IPR01254; Pept.Idae_S1_S6.
 DR InterPro: IPR001314; Peptidase_SIA.
 DR InterPro: IPR003966; Peptidase_SIA_pr.
 DR Pfam; PF00051; Kringle_5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; Trypsin_1.
 DR PRSF; P1SF001150; Plasmin; 1.
 DR PRINTS; PRO0722; CHMOTRIPPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR PRINTS; PRO1505; PROTHROMBIN.
 DR PRODOM; PD000395; Kringle_5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM0020; TRYPSIN_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00115; TRYPSIN_SER; 1.
 KW Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle; Plasma; Protease; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 KW SIGNAL. 1 19 By similarity.

FT	CHAIN	20	810	PIAmmingen.	
FT	PEPTIDE	20	582	Plasmin heavy chain A (By similarity).	
FT	CHAIN	98	582	Activation peptide (By similarity).	
FT	DOMAIN	583	810	Plasmin heavy chain A, short form (By similarity).	
FT	DOMAIN	20	98	Plasmin light chain B (By similarity).	
FT	DOMAIN	103	181	PAN.	
FT	ACT SITE	185	262	Kringle 1.	
FT	DOMAIN	275	352	Kringle 2.	
FT	DOMAIN	379	456	Kringle 3.	
FT	CARBOHYD	482	561	Kringle 4.	
FT	DOMAIN	582	808	Kringle 5.	
FT	DISULFID	583	61	Peptidase S1.	
FT	DISULFID	622	622	Charge relay system.	
FT	ACT SITE	665	655	Charge relay system.	
FT	ACT SITE	760	760	Charge relay system.	
FT	CARBOHYD	339	339	N-linked (GlcNAc . . .) (Potential).	
FT	DISULFID	49	73	By similarity.	
FT	DISULFID	52	61	By similarity.	
FT	DISULFID	103	181	By similarity.	
FT	DISULFID	124	164	By similarity.	
FT	DISULFID	152	176	By similarity.	
FT	DISULFID	185	262	By similarity.	
FT	DISULFID	188	316	By similarity.	
FT	DISULFID	206	245	By similarity.	
FT	DISULFID	234	257	By similarity.	
FT	DISULFID	275	352	By similarity.	
FT	DISULFID	296	335	By similarity.	
FT	DISULFID	324	347	By similarity.	
FT	DISULFID	379	456	By similarity.	
FT	DISULFID	400	439	By similarity.	
FT	DISULFID	428	451	By similarity.	
FT	DISULFID	482	561	By similarity.	
FT	DISULFID	503	544	By similarity.	
FT	DISULFID	532	556	By similarity.	
FT	DISULFID	569	685	Interchain (between A and B chains) (By similarity).	
FT	DISULFID	579	586	Interchain (between A and B chains) (By similarity).	
FT	DISULFID	607	623	By similarity.	
FT	DISULFID	699	766	By similarity.	
FT	DISULFID	729	745	By similarity.	
FT	DISULFID	756	784	By similarity.	
SQ	SEQUENCE	810 AA;	93902 MW;	68757809460/7A16 CRC64;	
Query Match		80.3%	Score 1237; DB 1; Length 810;		
Best Local Similarity		77.9%	Pred. No. 1.1e-85; Indels 0; Gaps 0;		
Matches		201;	Conservative 26; Mismatches 31; Delins 0; Gaps 0;		
Qy	1	VYLSECKTGKNGKTYGTMSTKNGITCQKNSSTSFRPRSPATHPSSEGLENYCNPDN 60	Qy	1	VYLSECKTGKNGKTYGTMSTKNGITCQKNSSTSFRPRSPATHPSSEGLENYCNPDN 60
Db	98	MVYLSCEKGKNGKTYGTMSTKNGITCQKNSSTSFRPRSPATHPSSEGLENYCNPDN 157	Db	81	VYLSECKTGKNGKTYGTMSTKNGITCQKNSSTSFRPRSPATHPSSEGLENYCNPDN 140
Qy	61	DPOQGWCYTDPDEKRYDCILRCEBECMCSGENYDGKISKTMGLCGQWADQSOPHAH 120	Qy	61	DPOQGWCYTDPDEKRYDCILRCEBECMCSGENYDGKISKTMGLCGQWADQSOPHAH 120
Db	158	DPKGPWCYTDPDEKRYDCILRCEBECMCSGENYDGKISKTMGLCGQWADQSOPHAH 217	Db	141	DBQGWCYTDPDEKRYDCILRCEBECMCSGENYDGKISKTMGLCGQWADQSOPHAH 200
Qy	181	GIGENYRGNVAVTISGHTQHWSQTQPTPHERTIPENPKQLDNEYCRNPDGKRPWCH 240	Qy	167	-----TPPPSSGPTQVCLKGTTGENYRGNVAVTWSGTQHWSAQPTPHB 211
Db	278	GNQKHYQGIVAVTWSGLTCQRWGQSPHRDRPENYPCKNLDEMYCRNPDGKRPWCH 258	Db	261	IIFIIIFIIFIMPLPLKGSSL---GRGENYRGNVAVTWSGTQHWSAQPTPHB 166
Qy	241	TNSQVRWEVKITSQDS 258	Db	201	GYPKSKPKNLDEMYCRNPDGKRPWCHTTSQVREYCKPSQDS 260
Db	338	TNSVRWEVKIPSQDS 355	Qy	171	RTPENPKKNLDEMYCRNPDGKRPWCHTTSQVREYCKPSQDS 316
Qy	121	GYPSKSKPKNLDEMYCRNPDGKRPWCHTTSQVREYCKPSQDS 337	Qy	121	GYPSKSKPKNLDEMYCRNPDGKRPWCHTTSQVREYCKPSQDS 363

RESULT 13
Q7TP84 RAT
ID Q7TP84_RAT PRELIMINARY; PRT; 759 AA.

GN	Name=PIG;
OS	Macropus; eugenii (Tasman wallaby).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TAXID	=9315;
[1]	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Liver;
RX	MSMLINE=9804511; PubMed=9342350; DOI=10.1073/pnas.94.22.11992;
RA	Lawn R.M.; Schwartz K.; Patti L.;
RT	"Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997 (1997).
CC	-1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor (By similarity).
CC	-1- CARBILIC ACTIVITY: Preferential cleavage: Lys- -Xaa > Arg- -Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.
CC	-1- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Activated with catalytic amounts of streptokinase (By similarity).
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-576, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
CC	-1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot (By similarity).
CC	-1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.
CC	-1- SIMILARITY: Contains 5 kringle domains.
CC	-1- SIMILARITY: Contains 1 PAN domain.
CC	-1- SIMILARITY: Contains 1 peptidase S1 domain.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
DR	EMBL; AF012297; AAB65760.1; - ; mRNA.
DR	HSSP; P00747; 1BUT.
DR	SMR; 01873; 561-806.
DR	MEROPS; S01.233; -.
DR	InterPro; IPR00001; Kringle.
DR	InterPro; IPR03014; PAN.
DR	InterPro; IPR03609; PAN_APP.
DR	InterPro; IPR01358; Peptidase_SIA_Plamin.
DR	InterPro; IPR01254; Peptidase_SIA_S6.
DR	InterPro; IPR001314; Peptidase_SIA.
DR	InterPro; IPR03966; Peptidase_SIA_Pr.
DR	Pfam; PF00051; Kringle; 5.
DR	Pfam; PF00024; PAN; 1.
DR	Pfam; PF00089; Trypsin; 1.
DR	Pfam; PF000150; Plasmin; 1.
DR	PRINTS; PR00722; CHMOTRIPSIN.
DR	PRINTS; PR00018; KRINGLE.
DR	PRINTS; PR0155; PROTHROMBIN.
DR	ProDom; PD000395; Kringle; 5.
Query	Query Match 75.3%; Score 1160; DB 1; Length 806; Best Local Similarity 71.7%; Pred. No. 7.9e-80; Matches 185; Conservative 34; Mismatches 39; Indels 0; Gaps 0;
Qy	1 VVLSCEKTTNGKNTGRTGMSTKKGCTCQNSSTSPPHRPFSPATHPSGLENTCRNPDN 60
Db	98 YISDCKSGNGRDKTTSKTKSGTCOKWSDSPHVPVKAAPSXPYDAGLEKNYCRNPDD 157
Qy	61 DPOQPMWCYTIDPEKRYDKDILEBEBECMHSGENGDGKSKITMSGLEQAMDSQPH 120
Db	158 DVKGWCWYCITNDPDIRYEVCDVPGEDCEMCSSGENYRGTKTSRSGIEQPWSQEPHS 217
Qy	121 GYPSKFPNPKNKKYCRNPDRRELPRWCFTDPNPKRMELCDIPRCTPPPSGSPYQCLK 180
Db	218 FYPFSKFPKSLDKIENYCRNPDRGEPRPWCFTSNPEKRWFCNIPRSSSSPPPGPMLQCLK 277
Qy	181 GTGEVTRGNVAVTWSHTCOHWSAQTPHTERTENPKCKLDENYCRPDRGKAPWCH 240

Db	277	GRGENTRGKIAVTKSQTICRNQKOPHKHNRTPENPCRGSDENYCRNPDCGELEPWCYT	337
Qy	241	TNSQVRWEYCKIPSCSS	258
Db	338	TNPDVQBYCAIPSCGS	355
RESULT	15		
Q6PBK6	BRARE		
ID	Q6PBK6_BRARE	PRELIMINARY;	PRT; 818 AA.
AC	Q6PBK6;		
DT	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DR	Plasminogen.		
GN	Name=Pig;		
OS	Brachydanio rerio (zebrafish) (Danio rerio).		
OC	Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OX	Cyprinidae; Danio.		
RN	NCBI_TAXID=7955;		
RC	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RT	TISSUE=Embryo;		
RA	NCBI-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,		
RA	Rao R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,		
RA	Brownstein M.J., Usdin T.B., Yoshiroki S., Carinci P., Prange C.,		
RA	Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McWayne C.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia J.M., Gay L.J., Kulyk S.W.,		
RA	Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahrey J., Heitman E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko A., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,		
RA	Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human .		
RT	and mouse cDNA sequences ",		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RL	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Embryo;		
RA	Straussberg R.;		
RA	Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.		
RL	EMBL: BC059801; AAH59801.1; -; mRNA.		
HSSP	P00747; IBI2.		
ZFIN	ZDB-GENB-030131-1411; plg;		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO; GO:000823; F:peptidase activity; IEA.		
DR	GO; GO:0004283; F:plasmin activity; IEA.		
DR	GO; GO:0003809; F:thrombin activity; IEA.		
DR	GO; GO:004295; F:trypsin activity; IEA.		
DR	GO; GO:0007596; F:blood coagulation; IEA.		
DR	GO; GO:0050874; P:organismal physiological process; IEA.		
DR	GO; GO:0006508; P:proteolysis and Peptidolysis; IEA.		
DR	InterPro; IPR000001; Kringle.		
DR	InterPro; IPR01358; PAN_APP.		
DR	InterPro; IPR01358; Pept_SIA_Plasm.		
DR	InterPro; IPR001254; Peptidase_S1_S6.		
DR	InterPro; IPR01314; Peptidase_SIA.		
DR	InterPro; IPR003966; Peptidase_SIA_pr.		
DR	Pfam; PF00051; Kringle; 5.		
DR	Pfam; PF00024; PAN; 1.		
DR	Pfam; PF00089; Trypsin; 1.		

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